

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: May 7, 2004, 17:24:39 ; Search time 59 Seconds  
(without alignments)  
2504.616 Million cell updates/sec

Title: US-10-017-867A-282  
Perfect score: 2768  
Sequence: 1 MAGQRVLLLVGFLLPGVLLS.....GKLLGMAVWWLRGARKVKET 523

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_29Jan04:\*  
1: geneseqp1980s:\*  
2: geneseqp1990s:\*  
3: geneseqp2000s:\*  
4: geneseqp2001s:\*  
5: geneseqp2002s:\*  
6: geneseqp2003as:\*  
7: geneseqp2003bs:\*  
8: geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	2768	100.0	523	3	AAB24025	Aab24025 Human PRO
2	2768	100.0	523	3	AAY99419	Aay99419 Human PRO
3	2768	100.0	523	4	AAB66168	Aab66168 Protein o
4	2768	100.0	523	6	ABO33661	Abo33661 Novel hum
5	2768	100.0	523	7	ABO44514	Abo44514 Human sec
6	2768	100.0	523	7	ABO33538	Abo33538 Novel hum
7	2768	100.0	523	7	ADC18151	Adc18151 Human PRO
8	2768	100.0	523	7	ADD70797	Add70797 Human sec
9	2768	100.0	523	7	ADD39874	Add39874 Human sec

10	2768	100.0	523	7	ADD70320	Add70320	Human	sec
11	2768	100.0	523	7	ADD38441	Add38441	Human	sec
12	2768	100.0	523	7	ADD39397	Add39397	Human	sec
13	2768	100.0	523	7	ADD38920	Add38920	Human	sec
14	2768	100.0	523	7	ADD40351	Add40351	Human	sec
15	2768	100.0	523	7	ADE50572	Ade50572	Human	sec
16	2768	100.0	523	7	ADE20184	Ade20184	Human	sec
17	2768	100.0	523	7	ADE50095	Ade50095	Human	sec
18	2768	100.0	523	7	ADE21653	Ade21653	Human	sec
19	2754	99.5	523	4	AAB88348	Aab88348	Human	mem
20	2547	92.0	489	5	AAO22789	Aao22789	Protein	o
21	2198	79.4	523	4	AAE02629	Aae02629	Human	sec
22	2198	79.4	523	5	AAE16939	Aae16939	Human	UDP
23	2198	79.4	523	5	ABB80590	Abb80590	Human	sbg
24	2194	79.3	523	5	AAE15435	Aae15435	Human	dru
25	2193	79.2	523	6	ADA55359	Ada55359	Human	pro
26	2191	79.2	523	5	ABG31867	Abg31867	Human	dru
27	1823	65.9	523	4	AAE02630	Aae02630	Mouse	sec
28	1751	63.3	393	5	ABB80589	Abb80589	Human	sbg
29	1294	46.7	526	4	ABG20645	Abg20645	Novel	hum
30	1142	41.3	318	4	ABB12293	Abb12293	Human	PRO
31	963	34.8	221	7	ADB64627	Adb64627	Human	pro
32	716.5	25.9	527	5	ABP71237	Abp71237	Human	326
33	714.5	25.8	527	4	AAU29284	Aau29284	Human	PRO
34	714.5	25.8	527	5	AAU77927	Aau77927	Human	dru
35	714.5	25.8	527	5	AAE15434	Aae15434	Human	dru
36	714.5	25.8	527	6	ABU58660	Abu58660	Human	PRO
37	714.5	25.8	527	6	ABU88208	Abu88208	Novel	hum
38	714.5	25.8	527	6	ABU84523	Abu84523	Human	sec
39	714.5	25.8	527	6	ABR66397	Abr66397	Human	sec
40	714.5	25.8	527	6	ABR65787	Abr65787	Human	sec
41	714.5	25.8	527	6	ABU99727	Abu99727	Human	sec
42	714.5	25.8	527	6	ABU82966	Abu82966	Human	PRO
43	714.5	25.8	527	6	ABU90087	Abu90087	Novel	hum
44	714.5	25.8	527	6	ABR68336	Abr68336	Human	sec
45	714.5	25.8	527	6	ABU96389	Abu96389	Novel	hum

# ALIGNMENTS

## RESULT 1

AAB24025

ID AAB24025 standard; protein; 523 AA.

XX

AC AAB24025;

XX

DT 25-JAN-2001 (first entry)

XX

DE Human PRO1780 protein sequence SEQ ID NO:13.

XX

KW Human; tumour; diagnosis; neoplastic disease; proliferation; cancer;

KW identification; tumorigenesis; anticancer; detection.

XX

OS Homo sapiens.

XX

PN WO200053750-A1.

XX  
PD 14-SEP-2000.  
XX  
PF 02-DEC-1999; 99WO-US028551.  
XX  
PR 08-MAR-1999; 99WO-US005028.  
PR 01-SEP-1999; 99WO-US020111.  
PR 29-OCT-1999; 99US-0162506P.  
PR 30-NOV-1999; 99WO-US028313.  
PR 01-DEC-1999; 99WO-US028634.  
XX  
PA (GETH ) GENENTECH INC.  
XX  
PI Botstein D, Goddard A, Gurney AL, Roy MA, Watanabe CK, Wood WI;  
XX  
DR WPI; 2000-594320/56.  
DR N-PSDB; AAC58107.  
XX  
PT Antibodies specific for PRO polypeptides, used to diagnose and inhibit  
PT the growth of tumors in mammals, and to identify inhibitors of PRO  
PT polypeptide activity or expression.  
XX  
PS Claim 61; Fig 10; 226pp; English.  
XX  
CC The present invention describes an antibody that binds to a human protein  
CC (I) selected from: PRO381; PRO1269; PRO1410; PRO1755; PRO1780; PRO3434;  
CC PRO1927; PRO3567; PRO1295; PRO1293; PRO1303; PRO4344; PRO4354; PRO4397;  
CC PRO4407; PRO1555; PRO1096; PRO2038; and PRO2262. (I) has anticancer  
CC activity and can be used to diagnose tumours in mammals, by detecting  
CC complex formation when the antibody is contacted with test cells.  
CC Increased expression of genes encoding (I) can also be detected to  
CC diagnose tumours. Agents which inhibit the activity of (I), especially  
CC the antibodies, or an antisense oligonucleotide which hybridises to genes  
CC encoding (I), can be used to inhibit tumour growth, preferably by  
CC inducing cell death. Methods from the present invention can be used to  
CC identify compounds which inhibit the biological activity of (I). AAC58019  
CC to AAC58102 represent PCR primers and hybridisation probes used in  
CC examples from the present invention for human PRO sequences. AAC58103 to  
CC AAC58122 and AAB24021 to AAB24040 represent human PRO polynucleotide and  
CC protein sequences given in the exemplification of the present invention  
XX  
SQ Sequence 523 AA;

Query Match 100.0%; Score 2768; DB 3; Length 523;  
Best Local Similarity 100.0%; Pred. No. 6.3e-278;  
Matches 523; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAGQRVLLLVGFLLPGVLLSEAAKILTISTVGGSHYLLMDRVSQILQDHGHNVTMLNHKR 60  
|  
Db 1 MAGQRVLLLVGFLLPGVLLSEAAKILTISTVGGSHYLLMDRVSQILQDHGHNVTMLNHKR 60  
  
Qy 61 GPFMPDFKKEEKSYQVISWLAPEDHQREFKKSFDFFLEETLGGRGKFENLLNVLEYLALQ 120  
|  
Db 61 GPFMPDFKKEEKSYQVISWLAPEDHQREFKKSFDFFLEETLGGRGKFENLLNVLEYLALQ 120  
  
Qy 121 CSHFLNRKDIMDSLKNENFDMVIVETFDYCPFLIAEKLGKPFVAILSTSFGSLEFGLPIP 180  
|

Db	121	CSHFLNRKDIMDSLKNENFDMVIVETFDYCPFLIAEKLGKPFVAILSTSFGSLEFGLPIP	180
Qy	181	LSYVPVFRSLLTDHMDFWGRVKNFLMFFSFCRRQQHMQSTFDNTIKEHFTEGSRPVLSHL	240
Db	181	LSYVPVFRSLLTDHMDFWGRVKNFLMFFSFCRRQQHMQSTFDNTIKEHFTEGSRPVLSHL	240
Qy	241	LLKAELWFINSDFAFDFAFARPLLNTVYVGGLMEKPIKPVPQDLENFIAKFGDSGFVLVTL	300
Db	241	LLKAELWFINSDFAFDFAFARPLLNTVYVGGLMEKPIKPVPQDLENFIAKFGDSGFVLVTL	300
Qy	301	GSMVNTCQNPEIFKEMNNAFAHLPGQVIWKCQCShWPKDVHLAANVKIVDWLPQSDLLAH	360
Db	301	GSMVNTCQNPEIFKEMNNAFAHLPGQVIWKCQCShWPKDVHLAANVKIVDWLPQSDLLAH	360
Qy	361	PSIRLFVTHGGQNSIMEAIQHGVP MVGIPLFGDQPENMVRVEAKKFGVSIQLKKLKAETL	420
Db	361	PSIRLFVTHGGQNSIMEAIQHGVP MVGIPLFGDQPENMVRVEAKKFGVSIQLKKLKAETL	420
Qy	421	ALKMKQIMEDKRYKSAAVAASVILRSHPLSPTQRLVGWIDHVLQTGGATHLKPYVFQQPW	480
Db	421	ALKMKQIMEDKRYKSAAVAASVILRSHPLSPTQRLVGWIDHVLQTGGATHLKPYVFQQPW	480
Qy	481	HEQYLFDFVVFLLGLTLGTLWL CGKLLGMAVWWLRGARKVKET	523
Db	481	HEQYLFDFVVFLLGLTLGTLWL CGKLLGMAVWWLRGARKVKET	523

RESULT 2

AA99419

ID AAY99419 standard; protein; 523 AA.

XX

AC AAY99419;

XX

DT 08-AUG-2000 (first entry)

XX

DE Human PRO1780 (UNQ842) amino acid sequence SEQ ID NO:282.

XX

KW Human; PRO polypeptide; membrane bound protein; receptor; diagnosis;  
KW transmembrane; secretion; immunoadhesion; pharmaceutical; screening.

XX

OS Homo sapiens.

XX

PN WO200012708-A2.

XX

PD 09-MAR-2000.

XX

PF 01-SEP-1999; 99WO-US020111.

XX

PR 01-SEP-1998; 98US-0098716P.

PR 01-SEP-1998; 98US-0098749P.

PR 01-SEP-1998; 98US-0098750P.

PR 02-SEP-1998; 98US-0098803P.

PR 02-SEP-1998; 98US-0098821P.

PR 02-SEP-1998; 98US-0098843P.

PR 09-SEP-1998; 98US-0099536P.

PR 09-SEP-1998; 98US-0099596P.

PR 09-SEP-1998; 98US-0099598P.



PR	09-SEP-1998;	98US-0099602P.
PR	09-SEP-1998;	98US-0099642P.
PR	10-SEP-1998;	98US-0099741P.
PR	10-SEP-1998;	98US-0099754P.
PR	10-SEP-1998;	98US-0099763P.
PR	10-SEP-1998;	98US-0099792P.
PR	10-SEP-1998;	98US-0099808P.
PR	10-SEP-1998;	98US-0099812P.
PR	10-SEP-1998;	98US-0099815P.
PR	10-SEP-1998;	98US-0099816P.
PR	15-SEP-1998;	98US-0100385P.
PR	15-SEP-1998;	98US-0100388P.
PR	15-SEP-1998;	98US-0100390P.
PR	16-SEP-1998;	98US-0100584P.
PR	16-SEP-1998;	98US-0100627P.
PR	16-SEP-1998;	98US-0100661P.
PR	16-SEP-1998;	98US-0100662P.
PR	16-SEP-1998;	98US-0100664P.
PR	17-SEP-1998;	98US-0100683P.
PR	17-SEP-1998;	98US-0100684P.
PR	17-SEP-1998;	98US-0100710P.
PR	17-SEP-1998;	98US-0100711P.
PR	17-SEP-1998;	98US-0100919P.
PR	17-SEP-1998;	98US-0100930P.
PR	18-SEP-1998;	98US-0100848P.
PR	18-SEP-1998;	98US-0100849P.
PR	18-SEP-1998;	98US-0101014P.
PR	18-SEP-1998;	98US-0101068P.
PR	18-SEP-1998;	98US-0101071P.
PR	22-SEP-1998;	98US-0101279P.
PR	23-SEP-1998;	98US-0101471P.
PR	23-SEP-1998;	98US-0101472P.
PR	23-SEP-1998;	98US-0101474P.
PR	23-SEP-1998;	98US-0101475P.
PR	23-SEP-1998;	98US-0101476P.
PR	23-SEP-1998;	98US-0101477P.
PR	23-SEP-1998;	98US-0101479P.
PR	24-SEP-1998;	98US-0101738P.
PR	24-SEP-1998;	98US-0101741P.
PR	24-SEP-1998;	98US-0101743P.
PR	24-SEP-1998;	98US-0101915P.
PR	24-SEP-1998;	98US-0101916P.
PR	29-SEP-1998;	98US-0102207P.
PR	29-SEP-1998;	98US-0102240P.
PR	29-SEP-1998;	98US-0102307P.
PR	29-SEP-1998;	98US-0102330P.
PR	29-SEP-1998;	98US-0102331P.
PR	30-SEP-1998;	98US-0102484P.
PR	30-SEP-1998;	98US-0102487P.
PR	30-SEP-1998;	98US-0102570P.
PR	30-SEP-1998;	98US-0102571P.
PR	01-OCT-1998;	98US-0102684P.
PR	01-OCT-1998;	98US-0102687P.
PR	02-OCT-1998;	98US-0102965P.
PR	06-OCT-1998;	98US-0103258P.
PR	06-OCT-1998;	98US-0103449P.
PR	07-OCT-1998;	98US-0103314P.

PR 07-OCT-1998; 98US-0103315P.  
PR 07-OCT-1998; 98US-0103328P.  
PR 07-OCT-1998; 98US-0103395P.  
PR 07-OCT-1998; 98US-0103396P.  
PR 07-OCT-1998; 98US-0103401P.  
PR 08-OCT-1998; 98US-0103633P.  
PR 08-OCT-1998; 98US-0103678P.  
PR 08-OCT-1998; 98US-0103679P.  
PR 08-OCT-1998; 98US-0103711P.  
PR 14-OCT-1998; 98US-0104257P.  
PR 20-OCT-1998; 98US-0104987P.  
PR 20-OCT-1998; 98US-0105000P.  
PR 20-OCT-1998; 98US-0105002P.  
PR 21-OCT-1998; 98US-0105104P.  
PR 22-OCT-1998; 98US-0105169P.  
PR 22-OCT-1998; 98US-0105266P.  
PR 26-OCT-1998; 98US-0105693P.  
PR 26-OCT-1998; 98US-0105694P.  
PR 27-OCT-1998; 98US-0105807P.  
PR 27-OCT-1998; 98US-0105881P.  
PR 27-OCT-1998; 98US-0105882P.  
PR 27-OCT-1998; 98US-0106062P.  
PR 28-OCT-1998; 98US-0106023P.  
PR 28-OCT-1998; 98US-0106029P.  
PR 28-OCT-1998; 98US-0106030P.  
PR 28-OCT-1998; 98US-0106032P.  
PR 28-OCT-1998; 98US-0106033P.  
PR 28-OCT-1998; 98US-0106178P.  
PR 29-OCT-1998; 98US-0106248P.  
PR 29-OCT-1998; 98US-0106384P.  
PR 29-OCT-1998; 98US-0108500P.  
PR 30-OCT-1998; 98US-0106464P.  
PR 03-NOV-1998; 98US-0106856P.  
PR 03-NOV-1998; 98US-0106902P.  
PR 03-NOV-1998; 98US-0106905P.  
PR 03-NOV-1998; 98US-0106919P.  
PR 03-NOV-1998; 98US-0106932P.  
PR 03-NOV-1998; 98US-0106934P.  
PR 10-NOV-1998; 98US-0107783P.  
PR 17-NOV-1998; 98US-0108775P.  
PR 17-NOV-1998; 98US-0108779P.  
PR 17-NOV-1998; 98US-0108787P.  
PR 17-NOV-1998; 98US-0108788P.  
PR 17-NOV-1998; 98US-0108801P.  
PR 17-NOV-1998; 98US-0108802P.  
PR 17-NOV-1998; 98US-0108806P.  
PR 17-NOV-1998; 98US-0108807P.  
PR 17-NOV-1998; 98US-0108867P.  
PR 17-NOV-1998; 98US-0108925P.  
PR 18-NOV-1998; 98US-0108848P.  
PR 18-NOV-1998; 98US-0108849P.  
PR 18-NOV-1998; 98US-0108850P.  
PR 18-NOV-1998; 98US-0108851P.  
PR 18-NOV-1998; 98US-0108852P.  
PR 18-NOV-1998; 98US-0108858P.  
PR 18-NOV-1998; 98US-0108904P.

XX

PA (GETH ) GENENTECH INC.  
 XX  
 PI Baker K, Goddard A, Gurney AL, Smith V, Watanabe CK, Wood WI;  
 XX  
 DR WPI; 2000-237871/20.  
 DR N-PSDB; AAA37101.  
 XX  
 PT New mammalian DNA sequences encoding transmembrane, receptor or secreted  
 PT PRO polypeptides, useful for screening of potential peptide or small  
 PT molecule inhibitors of the relevant receptor/ligand interactions.  
 XX  
 PS Claim 12; Fig 160; 773pp; English.  
 XX  
 CC AAA37022 to AAA37144 encode the new isolated human transmembrane,  
 CC receptor or secreted PRO polypeptides given in AAY99340 to AAY99462. The  
 CC transmembrane and receptor PRO proteins can be used for screening of  
 CC potential peptide or small molecule inhibitors of the relevant  
 CC receptor/ligand interactions. The polypeptides and nucleotide sequences  
 CC encoding then have various industrial applications, including uses as  
 CC pharmaceutical and diagnostic agents. AAA37145 to AAA37330 represent PCR  
 CC primers and hybridisation probes used in the isolation of the PRO  
 CC polypeptides from the present invention  
 XX  
 SQ Sequence 523 AA;

Query Match 100.0%; Score 2768; DB 3; Length 523;  
 Best Local Similarity 100.0%; Pred. No. 6.3e-278;  
 Matches 523; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MAGQRVLLLVGFLLPGVLLSEAAKILTISTVGGSHYLLMDRVSQILQDHGHNVTMLNHKR	60
Db	1	MAGQRVLLLVGFLLPGVLLSEAAKILTISTVGGSHYLLMDRVSQILQDHGHNVTMLNHKR	60
Qy	61	GPFMPDFKKEEKSYQVISWLAPEDHQREFKKSFDFLEETLGGRGKFENLLNVLEYLALQ	120
Db	61	GPFMPDFKKEEKSYQVISWLAPEDHQREFKKSFDFLEETLGGRGKFENLLNVLEYLALQ	120
Qy	121	CSHFLNRKDIMDSLKNENFDMVIVETFDYCPFLIAEKLKGKPFVAILSTSFGSLEFGLPIP	180
Db	121	CSHFLNRKDIMDSLKNENFDMVIVETFDYCPFLIAEKLKGKPFVAILSTSFGSLEFGLPIP	180
Qy	181	LSYVPVFRSLLTDHMDFWGRVKNFLMFFSFCRRQQHMQSTFDNTIKEHFTEGSRPVLSHL	240
Db	181	LSYVPVFRSLLTDHMDFWGRVKNFLMFFSFCRRQQHMQSTFDNTIKEHFTEGSRPVLSHL	240
Qy	241	LLKAELWFINSDFAFDFARPLLENTVYVVGGLMEKPIKPVPQDLENFIAKFGDSGFVLVTL	300
Db	241	LLKAELWFINSDFAFDFARPLLENTVYVVGGLMEKPIKPVPQDLENFIAKFGDSGFVLVTL	300
Qy	301	GSMVNTCQNPEIFKEMNNAFAHLPGQVIWKQCQSHWPKDVHLAANVKIVDWLPQSDLLAH	360
Db	301	GSMVNTCQNPEIFKEMNNAFAHLPGQVIWKQCQSHWPKDVHLAANVKIVDWLPQSDLLAH	360
Qy	361	PSIRLFVTHGGQNSIMEAIQHGVPVVGIPVPLFGDQPENMVRVEAKKFGVSIQLKKLKAETL	420
Db	361	PSIRLFVTHGGQNSIMEAIQHGVPVVGIPVPLFGDQPENMVRVEAKKFGVSIQLKKLKAETL	420

Qy 421 ALKMKQIMEDKRYKSAAVAASVILRSHPLSPTQRLVGWIDHVLQTGGATHLKPYVFQQPW 480  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 421 ALKMKQIMEDKRYKSAAVAASVILRSHPLSPTQRLVGWIDHVLQTGGATHLKPYVFQQPW 480

Qy 481 HEQYLFDVVFVLLGLTLGTLWLCLGKLLGMAVWWLRGARKVKET 523  
 ||||||||||||||||||||||||||||||||||||||||  
 Db 481 HEQYLFDVVFVLLGLTLGTLWLCLGKLLGMAVWWLRGARKVKET 523

RESULT 3

AAB66168

ID AAB66168 standard; protein; 523 AA.

XX

AC AAB66168;

XX

DT 02-APR-2001 (first entry)

XX

DE Protein of the invention #80.

XX

KW Secreted; transmembrane; gene therapy.

XX

OS Unidentified.

XX

PN WO200078961-A1.

XX

PD 28-DEC-2000.

XX

PF 18-FEB-2000; 2000WO-US004342.

XX

PR 23-JUN-1999; 99US-0141037P.

PR 20-JUL-1999; 99US-0144758P.

PR 26-JUL-1999; 99US-0145698P.

PR 01-SEP-1999; 99WO-US020111.

PR 29-OCT-1999; 99US-0162506P.

PR 30-NOV-1999; 99WO-US028313.

PR 02-DEC-1999; 99WO-US028551.

PR 16-DEC-1999; 99WO-US030095.

PR 05-JAN-2000; 2000WO-US000219.

PR 06-JAN-2000; 2000WO-US000376.

XX

PA (GETH ) GENENTECH INC.

XX

PI Baker KP, Botstein D, Desnoyers L, Eaton DL, Ferrara N, Fong S;

PI Gao W, Goddard A, Godowski PJ, Grimaldi CJ, Gurney AL, Hillan KJ;

PI Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D, Watanabe CK;

PI Williams PM, Wood WI;

XX

DR WPI; 2001-071395/08.

XX

PT Secreted and transmembrane proteins and nucleic acids designated PRO,  
 PT useful as hybridization probes, in chromosome and gene mapping and gene  
 PT therapy.

XX

PS Claim 1; Fig 160; 787pp; English.

XX

CC The present invention relates to secreted and transmembrane proteins.

CC These proteins and the DNA encoding them may be used as hybridization

CC probes, in chromosome and gene mapping and in the generation of anti-  
CC sense RNA and DNA. They may also be used used to generate either  
CC transgenic animals or knockout animals which are in turn useful for  
CC development and screening of therapeutically useful reagents. The nucleic  
CC acids may also be used in gene therapy

XX

SQ Sequence 523 AA;

Query Match 100.0%; Score 2768; DB 4; Length 523;  
Best Local Similarity 100.0%; Pred. No. 6.3e-278;  
Matches 523; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 MAGQRVLLLVGFLLPGVLLSEAAKILTISTVGGSHYLLMDRVSQILQDHGHNVTMLNHKR 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MAGQRVLLLVGFLLPGVLLSEAAKILTISTVGGSHYLLMDRVSQILQDHGHNVTMLNHKR 60

Qy     61 GPFMPDFKKEEKSYQVISWLAPEDHQREFKKSFDFFLEETLGGRGKFENLLNVLEYLALQ 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 GPFMPDFKKEEKSYQVISWLAPEDHQREFKKSFDFFLEETLGGRGKFENLLNVLEYLALQ 120

Qy    121 CSHFLNRKDIMDSLKNENFDMVIVETFDYCPFLIAEKLGPFFVAILSTSFGSLEFGLPIP 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 CSHFLNRKDIMDSLKNENFDMVIVETFDYCPFLIAEKLGPFFVAILSTSFGSLEFGLPIP 180

Qy    181 LSYVPVFRSLLTDHMDFWGRVKNFLMFFSFCRRQQHMQSTFDNTIKEHFTEGSRPVLSHL 240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 LSYVPVFRSLLTDHMDFWGRVKNFLMFFSFCRRQQHMQSTFDNTIKEHFTEGSRPVLSHL 240

Qy    241 LLKAELWFINSDFAFDFARPLLNTVYVGGLMEKPIKPVPQDLENFIAKFGDSGFVLVTL 300
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 LLKAELWFINSDFAFDFARPLLNTVYVGGLMEKPIKPVPQDLENFIAKFGDSGFVLVTL 300

Qy    301 GSMVNTCQNPEIFKEMNNAFAHLPQGVIWKCQCSHWPKDVHLAANVKIVDWLPQSDLLAH 360
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Qy    361 PSIRLFVTHGGQNSIMEAIQHGVPMVGIPFLFGDQPENMVRVEAKKFGVSIQLKKLKAETL 420
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Qy    481 HEQYLFDVVFVLLGLTLGTLWLWLCGKLLGMAVWWLRGARKVKET 523
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Db    481 HEQYLFDVVFVLLGLTLGTLWLWLCGKLLGMAVWWLRGARKVKET 523
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RESULT 4

ABO33661

ID ABO33661 standard; protein; 523 AA.

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AC ABO33661;

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DT 17-SEP-2003 (first entry)

XX

DE Novel human secreted and transmembrane protein PRO1780.  
 XX  
 KW Human; secreted and transmembrane protein; PRO; angiogenesis;  
 KW endothelial cell proliferation; wound healing; immune response;  
 KW T-lymphocytes proliferation; neonatal heart hypertrophy; tumour;  
 KW cardiac insufficiency disorder; calcium flux; inflammation;  
 KW vascular endothelial growth factor-stimulated proliferation;  
 KW mammalian kidney mesangial cell proliferation; Berger disease;  
 KW nephropathy; Schanlein-Henoch purpura; celiac disease; Crohn's disease;  
 KW dermatitis herpetiformis; diabetes; haemoglobin switch; insulinaemia;  
 KW pancreatic beta-cell precursor cell differentiation; thalassemias;  
 KW obesity; auditory hair cell regeneration; hearing loss; bone disorder;  
 KW cartilage disorder; sports injury; arthritis.  
 XX  
 OS Homo sapiens.  
 XX  
 PN US2003073130-A1.  
 XX  
 PD 17-APR-2003.  
 XX  
 PF 11-DEC-2001; 2001US-00015869.  
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PR 29-JUN-2001; 2001WO-US021066.  
PR 09-JUL-2001; 2001WO-US021735.  
PR 04-SEP-2001; 2001US-00946374.

XX

PA (GETH ) GENENTECH INC.

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PI Baker KP, Botstein D, Desnoyers L, Eaton DL, Ferrara N, Fong S;  
PI Gao W, Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;  
PI Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D, Watanabe CK;  
PI Williams PM, Wood WI;

XX

DR WPI; 2003-585293/55.

DR N-PSDB; ACD68440.

XX

PT Novel isolated PRO polypeptides e.g. PRO1130, PRO1275, PRO1418, PRO1555,  
PT PRO1787 that modulate glucose or free fatty acid uptake by skeletal  
PT muscle cells, and are useful for treating diabetes, hyper- or hypo-

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Matches 523; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 5

ABO44514

ID ABO44514 standard; protein; 523 AA.

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AC ABO44514;

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DT 01-OCT-2003 (first entry)

XX

DE Human secreted/transmembrane protein PRO1780.

XX

KW Human; secreted protein; transmembrane protein; PRO; vulnerary; cardiant;

KW antidiabetic; anorectic; antiarthritic; angiogenesis; cancer;

KW adrenal cortical capillary; endothelial cell growth; wound healing;

KW stimulated T-lymphocyte proliferation; immune response suppression;

KW neonatal heart hypertrophy; cardiac insufficiency disorder;

KW vascular endothelial growth factor; inflammation; mononuclear cell;

KW eosinophil; diabetes; obesity; or hyper-insulinaemia; hypo-insulinaemia;

KW chondrocyte redifferentiation; bone disorder; cartilage disorder;

KW sports injury; arthritis.

XX

OS Homo sapiens.

XX

PN US2003044841-A1.

XX

PD 06-MAR-2003.

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PF 06-DEC-2001; 2001US-00006856.

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 PR 20-JUN-2001; 2001WO-US019692.  
 PR 29-JUN-2001; 2001WO-US021066.  
 PR 09-JUL-2001; 2001WO-US021735.  
 PR 04-SEP-2001; 2001US-00946374.

XX

PA (GETH ) GENENTECH INC.

XX

PI Baker KP, Botstein D, Desnoyers L, Eaton DL, Ferrara N, Fong S;  
 PI Gao W, Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;  
 PI Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D, Watanabe CK;  
 PI Williams PM, Wood WI;

XX

DR WPI; 2003-492259/46.

DR N-PSDB; ACH04542.

XX

PT Novel secreted and transmembrane polypeptides and polynucleotides  
 PT encoding them useful for treating various cardiac insufficiency  
 PT disorders, bone and/or cartilage disorders such as sports injuries and  
 PT arthritis.

Query Match 100.0%; Score 2768; DB 7; Length 523;  
 Best Local Similarity 100.0%; Pred. No. 6.3e-278;  
 Matches 523; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAGQRVLLLVGFLLPGVLLSEAAKILTISTVGGSHYLLMDRVSQILQDHGHNVTMLNHKR 60  
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 Db 1 MAGQRVLLLVGFLLPGVLLSEAAKILTISTVGGSHYLLMDRVSQILQDHGHNVTMLNHKR 60  
 QY 61 GPFMPDFKKEEKSYQVISWLAPEDHQREFKKSFDFFLEETLGGRGKFENLLNVLEYLALQ 120  
 |||  
 Db 61 GPFMPDFKKEEKSYQVISWLAPEDHQREFKKSFDFFLEETLGGRGKFENLLNVLEYLALQ 120  
 QY 121 CSHFLNRKDIMDSLKNENFDMVIVETFDYCPFLIAEKLKGKPFVAILSTSFGSLEFGLPIP 180  
 |||  
 Db 121 CSHFLNRKDIMDSLKNENFDMVIVETFDYCPFLIAEKLKGKPFVAILSTSFGSLEFGLPIP 180  
 QY 181 LSYVPVFRSLLTDHMDFWGRVKNFLMFFSFCRRQOHMQSTFDNTIKEHFTEGSRPVLSHL 240

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Db      181  |||||LSYVPVFRSLLTDHMDFWGRVKNFLMFFSFCRRQQHMQSTFDNTIKEHFTEGSRPVLSHL 240
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Qy      301  GSMVNTCQNPEIFKEMNNAFAHLPQGVIWKCQCSHWPKDVHLAANVKIVDWLPQSDLLAH 360
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Qy      361  PSIRLFVTHGGQNSIMEAIQHGVPVMGIPLFGDQPENMVRVEAKKFGVSIQLKKLKAETL 420
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Qy      421  ALKMKQIMEDKRYKSAAVAASVILRSHPLSPTQRLVGWIDHVLQTGGATHLKPYPVFQQPW 480
Db      421  |||||ALKMKQIMEDKRYKSAAVAASVILRSHPLSPTQRLVGWIDHVLQTGGATHLKPYPVFQQPW 480
Qy      481  HEQYLFDFVFVFLGLTLGLTLWLCLGKLLGMAVWWLRGARKVKET 523
Db      481  |||||HEQYLFDFVFVFLGLTLGLTLWLCLGKLLGMAVWWLRGARKVKET 523

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RESULT 6

ABO33538

ID ABO33538 standard; protein; 523 AA.

XX

AC ABO33538;

XX

DT 17-SEP-2003 (first entry)

XX

DE Novel human secreted and transmembrane protein PRO1780.

XX

KW Human; secreted and transmembrane protein; PRO; gene therapy; vaccine;

KW tissue typing; chromosome identification; vaccine.

XX

OS Homo sapiens.

XX

PN US2003073129-A1.

XX

PD 17-APR-2003.

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PF 04-SEP-2001; 2001US-00946374.

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PR 01-SEP-1998; 98US-0098716P.

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PR 01-SEP-1998; 98US-0098750P.

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PR	22-DEC-1998;	98US-00218517.
PR	22-DEC-1998;	98US-0113296P.
PR	30-DEC-1998;	98US-0114223P.



PR 05-JAN-1999; 99WO-US000106.  
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PR 23-JUN-1999; 99US-0141037P.  
PR 20-JUL-1999; 99US-0144758P.  
PR 26-JUL-1999; 99US-0145698P.  
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PR 15-SEP-1999; 99WO-US021194.  
PR 18-OCT-1999; 99US-00403297.  
PR 30-NOV-1999; 99WO-US028313.  
PR 02-DEC-1999; 99WO-US028551.  
PR 16-DEC-1999; 99WO-US030095.  
PR 05-JAN-2000; 2000WO-US000219.  
PR 06-JAN-2000; 2000WO-US000376.  
PR 11-FEB-2000; 2000WO-US003565.  
PR 18-FEB-2000; 2000WO-US004342.  
PR 24-FEB-2000; 2000WO-US005004.  
PR 02-MAR-2000; 2000WO-US005841.  
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PR 17-MAY-2000; 2000WO-US013705.  
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PR 30-MAY-2000; 2000WO-US014941.  
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PR 23-AUG-2000; 2000WO-US023522.  
PR 24-AUG-2000; 2000WO-US023328.  
PR 08-NOV-2000; 2000WO-US030952.  
PR 10-NOV-2000; 2000WO-US030873.  
PR 01-DEC-2000; 2000WO-US032678.  
PR 28-FEB-2001; 2001WO-US006520.  
PR 01-MAR-2001; 2001WO-US006666.  
PR 01-JUN-2001; 2001US-00872035.  
PR 01-JUN-2001; 2001WO-US017800.  
PR 14-JUN-2001; 2001US-00882636.  
PR 20-JUN-2001; 2001WO-US019692.  
PR 29-JUN-2001; 2001WO-US021066.  
PR 09-JUL-2001; 2001WO-US021735.

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PA (GETH ) GENENTECH INC.

XX

PI Baker KP, Botstein D, Desnoyers L, Eaton DL, Ferrara N, Fong S;  
PI Gao W, Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;  
PI Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D, Watanabe CK;  
PI Williams PM, Wood WI;

XX

DR WPI; 2003-585292/55.

DR N-PSDB; ACD68086.

XX

PT Novel isolated PRO polypeptides e.g. PRO1491 and PRO1571, useful in the  
PT preparation of a medicament for treating a condition responsive to PRO  
PT polypeptide, and as therapeutic agents e.g. vaccines.

XX

PS Claim 12; Fig 160; 561pp; English.

XX

CC The invention describes an isolated PRO (secreted and transmembrane)  
CC polypeptide (I), having at least 80% sequence identity to a sequence

Query Match

100.0%; Score 2768; DB 7; Length 523;

Best Local Similarity 100.0%; Pred. No. 6.3e-278;  
Matches 523; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db      1 MAGQRVLLLVGFLLPGVLLSEAAKILTISTVGGSHYLLMDRVSQILQDHGHNVTMLNHKR 60

Qy     61 GPFMPDFKKEEKSYQVISWLAPEDHQREFKKSFDFFLEETLGGRGKFENLLNVLEYLALQ 120
        |||
Db     61 GPFMPDFKKEEKSYQVISWLAPEDHQREFKKSFDFFLEETLGGRGKFENLLNVLEYLALQ 120

Qy    121 CSHFLNRKDIMDSLKNENFDMVIVETFDYCPFLIAEKLGKPFVAILSTSFGSLEFGLPIP 180
        |||
Db    121 CSHFLNRKDIMDSLKNENFDMVIVETFDYCPFLIAEKLGKPFVAILSTSFGSLEFGLPIP 180

Qy    181 LSYVPVFRSLLTDHMDFWGRVKNFLMFFSFCRRQQHMQSTFDNTIKEHFTEGSRPVLSHL 240
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Qy    241 LLKAELWFINSDFAFDFARPLLNTVYVGGLMEKPIKPVPQDLENFIAKFGDSGFVLVTL 300
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Db    421 ALKMKQIMEDKRYKSAAVAASVILRSHPLSPTQRLVGWIDHVLQTGGATHLKPYVFQQPW 480

Qy    481 HEQYLFDFVFVFLGLTLGTLWLWLCGKLLGMAVWWLRGARKVKET 523
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Db    481 HEQYLFDFVFVFLGLTLGTLWLWLCGKLLGMAVWWLRGARKVKET 523
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RESULT 7

ADC18151

ID ADC18151 standard; protein; 523 AA.

XX

AC ADC18151;

XX

DT 18-DEC-2003 (first entry)

XX

DE Human PRO polypeptide #80.

XX

KW Human; PRO; protein electrophoresis; chromosome mapping; gene mapping;  
KW genetic disorder.

XX

OS Homo sapiens.

XX

PN US2003064925-A1.

XX

PD 03-APR-2003.  
XX  
PF 10-DEC-2001; 2001US-00013907.  
XX  
PR 01-SEP-1998; 98US-0098716P.  
PR 01-SEP-1998; 98US-0098723P.  
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PR 02-SEP-1998; 98US-0098803P.  
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PR 17-NOV-1998; 98US-0108806P.  
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PR 30-DEC-1998; 98US-0114223P.  
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PR 26-JUL-1999; 99US-0145698P.  
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PR 30-NOV-1999; 99WO-US028313.  
PR 02-DEC-1999; 99WO-US028551.  
PR 16-DEC-1999; 99WO-US030095.  
PR 05-JAN-2000; 2000WO-US000219.  
PR 06-JAN-2000; 2000WO-US000376.  
PR 11-FEB-2000; 2000WO-US003565.  
PR 18-FEB-2000; 2000WO-US004342.  
PR 24-FEB-2000; 2000WO-US005004.  
PR 02-MAR-2000; 2000WO-US005841.  
PR 15-MAR-2000; 2000WO-US006884.  
PR 17-MAY-2000; 2000WO-US013705.  
PR 22-MAY-2000; 2000WO-US014042.  
PR 30-MAY-2000; 2000WO-US014941.  
PR 02-JUN-2000; 2000WO-US015264.  
PR 23-AUG-2000; 2000WO-US023522.  
PR 24-AUG-2000; 2000WO-US023328.  
PR 08-NOV-2000; 2000WO-US030952.  
PR 10-NOV-2000; 2000WO-US030873.  
PR 01-DEC-2000; 2000WO-US032678.  
PR 28-FEB-2001; 2001WO-US006520.  
PR 01-MAR-2001; 2001WO-US006666.  
PR 01-JUN-2001; 2001WO-US017800.  
PR 20-JUN-2001; 2001WO-US019692.  
PR 29-JUN-2001; 2001WO-US021066.  
PR 09-JUL-2001; 2001WO-US021735.  
PR 04-SEP-2001; 2001US-00946374.

XX

PA (GETH ) GENENTECH INC.

XX

PI Baker KP, Botstein D, Desnoyers L, Eaton DL, Ferrara N, Fong S;  
PI Gao W, Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;  
PI Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D, Watanabe CK;  
PI Williams PM, Wood WI;

XX

DR WPI; 2003-555602/52.  
 DR N-PSDB; ADC18150.  
 XX  
 PT Novel isolated PRO polypeptides e.g. PRO1491 and PRO1571, useful in the  
 PT preparation of a medicament for treating a condition responsive to PRO  
 PT polypeptide, and as therapeutic agents e.g. vaccines.  
 XX  
 PS Claim 12; SEQ ID NO 282; 555pp; English.  
 XX  
 CC The invention relates to human PRO polypeptides and the polynucleotides  
 CC encoding them. The sequences are useful in the preparation of a  
 CC medicament for treating a condition responsive to a PRO polypeptide. The  
 CC polypeptides are useful in a number of functional biological assays, as  
 CC molecular weight markers for protein electrophoresis and as therapeutic

Query Match 100.0%; Score 2768; DB 7; Length 523;  
 Best Local Similarity 100.0%; Pred. No. 6.3e-278;  
 Matches 523; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MAGQRVLLLVGFLLPGVLLSEAAKILTISTVGGSHYLLMDRVSQILQDHGHNVMTLNHKR	60
Db	1	MAGQRVLLLVGFLLPGVLLSEAAKILTISTVGGSHYLLMDRVSQILQDHGHNVMTLNHKR	60
Qy	61	GPFMPDFKKEEKSQVISWLAPEDHQREFKKSFDFFLEETLGGRGKFENLLNVLEYLALQ	120
Db	61	GPFMPDFKKEEKSQVISWLAPEDHQREFKKSFDFFLEETLGGRGKFENLLNVLEYLALQ	120
Qy	121	CSHFLNRKDIMDSLKNENFDMVIVETFDYCPFLIAEKLGKPFVAILSTSFGSLEFGLPIP	180
Db	121	CSHFLNRKDIMDSLKNENFDMVIVETFDYCPFLIAEKLGKPFVAILSTSFGSLEFGLPIP	180
Qy	181	LSYVPVFRSLLTDHMDFWGRVKNFLMFFSFCCRQQHMOSTFDNTIKEHFTEGSRPVLSHL	240
Db	181	LSYVPVFRSLLTDHMDFWGRVKNFLMFFSFCCRQQHMOSTFDNTIKEHFTEGSRPVLSHL	240
Qy	241	LLKAELWFINSDFAFDFARPLLNPNTVYVGGLMEKPIKPVQDLENFIAKFGDSGFVLVTL	300
Db	241	LLKAELWFINSDFAFDFARPLLNPNTVYVGGLMEKPIKPVQDLENFIAKFGDSGFVLVTL	300
Qy	301	GSMVNTCQNPEIFKEMNNAFAHLPQGVIWKCQCSEHWPKDVHLAANVKIVDWLPQSDLLAH	360
Db	301	GSMVNTCQNPEIFKEMNNAFAHLPQGVIWKCQCSEHWPKDVHLAANVKIVDWLPQSDLLAH	360
Qy	361	PSIRLFVTHGGQNSIMEAIQHGVPVMVGIPLFGDQPENMVRVEAKKFGVSIQLKKLKAETL	420
Db	361	PSIRLFVTHGGQNSIMEAIQHGVPVMVGIPLFGDQPENMVRVEAKKFGVSIQLKKLKAETL	420
Qy	421	ALKMKQIMEDKRYKSAAVAASVILRSHPLSPTQRLVGWIDHVLQTGGATHLKPYVFQQPW	480
Db	421	ALKMKQIMEDKRYKSAAVAASVILRSHPLSPTQRLVGWIDHVLQTGGATHLKPYVFQQPW	480
Qy	481	HEQYLFDFVFVFLGLTLGLTLWLCGKLLGMAVWWLRGARKVKET	523
Db	481	HEQYLFDFVFVFLGLTLGLTLWLCGKLLGMAVWWLRGARKVKET	523

ADD70797

ID ADD70797 standard; protein; 523 AA.

XX

AC ADD70797;

XX

DT 15-JAN-2004 (first entry)

XX

DE Human secreted/transmembrane protein PRO1780.

XX

KW Human; secreted protein; transmembrane protein; PRO; tumour;

KW immune response; cardiac insufficiency disorder; calcium flux;

KW umbilical vein endothelial cell; bone disorder; cartilage disorder;

KW arthritis; wound healing; diabetes; skeletal muscle cells; obesity;

KW Berger disease; nephropathy; Schonlein-Henoch purpura; coeliac disease;

KW dermatitis; herpetiformis; Crohn's disease; thalassaemia.

XX

OS Homo sapiens.

XX

PN US2003099625-A1.

XX

PD 29-MAY-2003.

XX

PF 12-DEC-2001; 2001US-00015386.

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PR 01-SEP-1998; 98US-0098716P.

PR 01-SEP-1998; 98US-0098723P.

PR 01-SEP-1998; 98US-0098749P.

PR 01-SEP-1998; 98US-0098750P.

PR 02-SEP-1998; 98US-0098803P.

PR 02-SEP-1998; 98US-0098821P.

PR 02-SEP-1998; 98US-0098843P.

PR 09-SEP-1998; 98US-0099536P.

PR 09-SEP-1998; 98US-0099596P.

PR 09-SEP-1998; 98US-0099598P.

PR 09-SEP-1998; 98US-0099602P.

PR 09-SEP-1998; 98US-0099642P.

PR 10-SEP-1998; 98US-0099741P.

PR 10-SEP-1998; 98US-0099754P.

PR 10-SEP-1998; 98US-0099763P.

PR 10-SEP-1998; 98US-0099792P.

PR 10-SEP-1998; 98US-0099808P.

PR 10-SEP-1998; 98US-0099812P.

PR 10-SEP-1998; 98US-0099815P.

PR 10-SEP-1998; 98US-0099816P.

PR 15-SEP-1998; 98US-0100385P.

PR 15-SEP-1998; 98US-0100388P.

PR 15-SEP-1998; 98US-0100390P.

PR 16-SEP-1998; 98US-0100584P.

PR 16-SEP-1998; 98US-0100627P.

PR 16-SEP-1998; 98US-0100661P.

PR 16-SEP-1998; 98US-0100662P.

PR 16-SEP-1998; 98US-0100664P.

PR 17-SEP-1998; 98US-0100683P.

PR 17-SEP-1998; 98US-0100684P.

PR 17-SEP-1998; 98US-0100710P.

PR 17-SEP-1998; 98US-0100711P.

PR 17-SEP-1998; 98US-0100919P.

PR	17-SEP-1998;	98US-0100930P.
PR	18-SEP-1998;	98US-0100848P.
PR	18-SEP-1998;	98US-0100849P.
PR	18-SEP-1998;	98US-0101014P.
PR	18-SEP-1998;	98US-0101068P.
PR	18-SEP-1998;	98US-0101071P.
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PR	23-SEP-1998;	98US-0101472P.
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PR	23-SEP-1998;	98US-0101477P.
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PR	24-SEP-1998;	98US-0101738P.
PR	24-SEP-1998;	98US-0101741P.
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PR	24-SEP-1998;	98US-0101915P.
PR	24-SEP-1998;	98US-0101916P.
PR	29-SEP-1998;	98US-0102207P.
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PR	29-SEP-1998;	98US-0102330P.
PR	29-SEP-1998;	98US-0102331P.
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PR	30-SEP-1998;	98US-0102487P.
PR	30-SEP-1998;	98US-0102570P.
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PR	01-OCT-1998;	98US-0102684P.
PR	01-OCT-1998;	98US-0102687P.
PR	02-OCT-1998;	98US-0102965P.
PR	06-OCT-1998;	98US-0103258P.
PR	06-OCT-1998;	98US-0103449P.
PR	07-OCT-1998;	98US-0103314P.
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PR	07-OCT-1998;	98US-0103395P.
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PR	07-OCT-1998;	98US-0103401P.
PR	08-OCT-1998;	98US-0103633P.
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PR	14-OCT-1998;	98US-0104257P.
PR	20-OCT-1998;	98US-0104987P.
PR	20-OCT-1998;	98US-0105000P.
PR	20-OCT-1998;	98US-0105002P.
PR	21-OCT-1998;	98US-0105104P.
PR	22-OCT-1998;	98US-0105169P.
PR	22-OCT-1998;	98US-0105266P.
PR	26-OCT-1998;	98US-0105693P.
PR	26-OCT-1998;	98US-0105694P.
PR	27-OCT-1998;	98US-0105807P.
PR	27-OCT-1998;	98US-0105881P.
PR	27-OCT-1998;	98US-0105882P.
PR	27-OCT-1998;	98US-0106062P.
PR	28-OCT-1998;	98US-0106023P.



PR 28-OCT-1998; 98US-0106029P.  
PR 28-OCT-1998; 98US-0106030P.  
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PR 28-OCT-1998; 98US-0106033P.  
PR 28-OCT-1998; 98US-0106178P.  
PR 29-OCT-1998; 98US-0106248P.  
PR 29-OCT-1998; 98US-0106384P.  
PR 29-OCT-1998; 98US-0108500P.  
PR 30-OCT-1998; 98US-0106464P.  
PR 03-NOV-1998; 98US-0106856P.  
PR 03-NOV-1998; 98US-0106902P.  
PR 03-NOV-1998; 98US-0106905P.  
PR 03-NOV-1998; 98US-0106919P.  
PR 03-NOV-1998; 98US-0106932P.  
PR 03-NOV-1998; 98US-0106934P.  
PR 10-NOV-1998; 98US-0107783P.  
PR 17-NOV-1998; 98US-0108775P.  
PR 17-NOV-1998; 98US-0108779P.  
PR 17-NOV-1998; 98US-0108787P.  
PR 17-NOV-1998; 98US-0108788P.  
PR 17-NOV-1998; 98US-0108801P.  
PR 17-NOV-1998; 98US-0108802P.  
PR 17-NOV-1998; 98US-0108806P.  
PR 17-NOV-1998; 98US-0108807P.  
PR 17-NOV-1998; 98US-0108867P.  
PR 17-NOV-1998; 98US-0108925P.  
PR 18-NOV-1998; 98US-0108848P.  
PR 18-NOV-1998; 98US-0108849P.  
PR 18-NOV-1998; 98US-0108850P.  
PR 18-NOV-1998; 98US-0108851P.  
PR 18-NOV-1998; 98US-0108852P.  
PR 18-NOV-1998; 98US-0108858P.  
PR 18-NOV-1998; 98US-0108904P.  
PR 22-DEC-1998; 98US-0113296P.  
PR 30-DEC-1998; 98US-0114223P.  
PR 05-JAN-1999; 99WO-US000106.  
PR 16-APR-1999; 99US-0129674P.  
PR 23-JUN-1999; 99US-0141037P.  
PR 20-JUL-1999; 99US-0144758P.  
PR 26-JUL-1999; 99US-0145698P.  
PR 01-SEP-1999; 99WO-US020111.  
PR 15-SEP-1999; 99WO-US021194.  
PR 29-OCT-1999; 99US-0162506P.  
PR 30-NOV-1999; 99WO-US028313.  
PR 02-DEC-1999; 99WO-US028551.  
PR 16-DEC-1999; 99WO-US030095.  
PR 05-JAN-2000; 2000WO-US000219.  
PR 06-JAN-2000; 2000WO-US000376.  
PR 11-FEB-2000; 2000WO-US003565.  
PR 18-FEB-2000; 2000WO-US004342.  
PR 24-FEB-2000; 2000WO-US005004.  
PR 02-MAR-2000; 2000WO-US005841.  
PR 15-MAR-2000; 2000WO-US006884.  
PR 17-MAY-2000; 2000WO-US013705.  
PR 22-MAY-2000; 2000WO-US014042.  
PR 30-MAY-2000; 2000WO-US014941.  
PR 02-JUN-2000; 2000WO-US015264.

PR 23-AUG-2000; 2000WO-US023522.  
PR 24-AUG-2000; 2000WO-US023328.  
PR 08-NOV-2000; 2000WO-US030952.  
PR 10-NOV-2000; 2000WO-US030873.  
PR 01-DEC-2000; 2000WO-US032678.  
PR 28-FEB-2001; 2001WO-US006520.  
PR 01-MAR-2001; 2001WO-US006666.  
PR 01-JUN-2001; 2001WO-US017800.  
PR 20-JUN-2001; 2001WO-US019692.  
PR 29-JUN-2001; 2001WO-US021066.  
PR 09-JUL-2001; 2001WO-US021735.  
PR 04-SEP-2001; 2001US-00946374.

XX

PA (GETH ) GENENTECH INC.

XX

PI Baker KP, Botstein D, Desnoyers L, Eaton DL, Ferrara N, Fong S;  
PI Gao W, Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;  
PI Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D, Watanabe CK;  
PI Williams PM, Wood WI;

XX

DR WPI; 2003-874602/81.

DR N-PSDB; ADD70796.

XX

PT Novel isolated PRO polypeptides e.g., PRO1130, PRO1275, PRO1418, PRO1555,  
PT PRO1787 affect glucose or free fatty acid (FFA) uptake by skeletal muscle  
PT cells and are useful for treating diabetes or hyper- or hypo-insulinemia.

XX

PS Claim 12; SEQ ID NO 282; 553pp; English.

XX

CC The invention relates to an isolated PRO polypeptide (secreted or

Query Match 100.0%; Score 2768; DB 7; Length 523;  
Best Local Similarity 100.0%; Pred. No. 6.3e-278;  
Matches 523; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MAGQRVLLLVGFLLPGVLLSEAAKILTISTVGGSHYLLMDRVSQILQDHGHNVTMLNHKR	60
Db	1	MAGQRVLLLVGFLLPGVLLSEAAKILTISTVGGSHYLLMDRVSQILQDHGHNVTMLNHKR	60
Qy	61	GPFPMPDFKKEEKSYQVISWLAPEDHQREFKKSFDFFLEETLGGRGKFENLLNVLEYLALQ	120
Db	61	GPFPMPDFKKEEKSYQVISWLAPEDHQREFKKSFDFFLEETLGGRGKFENLLNVLEYLALQ	120
Qy	121	CSHFLNRKDIMDSLKNENFDMVIVETFDYCPFLIAEKLGKPFVAILSTSFGSLEFGLPIP	180
Db	121	CSHFLNRKDIMDSLKNENFDMVIVETFDYCPFLIAEKLGKPFVAILSTSFGSLEFGLPIP	180
Qy	181	LSYVPVFRSLLTDHMDFWGRVKNFLMFFSFERRQQHMQSTFDNTIKEHFTEGSRPVLSHL	240
Db	181	LSYVPVFRSLLTDHMDFWGRVKNFLMFFSFERRQQHMQSTFDNTIKEHFTEGSRPVLSHL	240
Qy	241	LLKAELWFINSDFAFDFARPLLNTVYVGGLMKPKPKVPQDLENFIAKFGDSGFVLVTL	300
Db	241	LLKAELWFINSDFAFDFARPLLNTVYVGGLMKPKPKVPQDLENFIAKFGDSGFVLVTL	300
Qy	301	GSMVNTCQNPEIFKEMNNAFAHLPQGVIWKQCShwPKDVHLAANVKIVDWLPQSDLLAH	360

Db 301 GSMVNTCQNPEIFKEMNNAFAHLPQGVIWKCQCSHWPKDVHLAANVKIVDWLPQSDLLAH 360

QY 361 PSIRLFVTHGGQNSIMEAIQHGVP MVGIP LFGDQ PENMVRVEAKKFGVSIQLKKLKAETL 420  
 |||

Db 361 PSIRLFVTHGGQNSIMEAIQHGVP MVGIP LFGDQ PENMVRVEAKKFGVSIQLKKLKAETL 420

QY 421 ALKMKQIMEDKRYKSAAVAASVILRSHPLSPTQRLVGWIDHVLQTGGATHLKPYVFQQPW 480  
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Db 421 ALKMKQIMEDKRYKSAAVAASVILRSHPLSPTQRLVGWIDHVLQTGGATHLKPYVFQQPW 480

QY 481 HEQYLFDFVFVFLGLTLGLTLWLCGKLLGMAVWWLRGARKVKET 523  
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Db 481 HEQYLFDFVFVFLGLTLGLTLWLCGKLLGMAVWWLRGARKVKET 523

RESULT 9

ADD39874

ID ADD39874 standard; protein; 523 AA.

XX

AC ADD39874;

XX

DT 15-JAN-2004 (first entry)

XX

DE Human secreted/transmembrane protein PRO1780.

XX

KW Human; secreted protein; transmembrane protein; PRO; tumour;

KW immune response; cardiac insufficiency disorder; calcium flux;

KW umbilical vein endothelial cell; bone disorder; cartilage disorder;

KW arthritis; wound healing; diabetes; skeletal muscle cells; obesity;

KW Berger disease; nephropathy; Schonlein-Henoch purpura; coeliac disease;

KW dermatitis; herpetiformis; Crohn's disease; thalassaemia.

XX

OS Homo sapiens.

XX

PN US2003083462-A1.

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PD 01-MAY-2003.

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PF 10-DEC-2001; 2001US-00013913.

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PR 05-JAN-1999; 99WO-US000106.

PR 01-SEP-1999; 99WO-US020111.

PR 15-SEP-1999; 99WO-US021194.

PR 30-NOV-1999; 99WO-US028313.

PR 02-DEC-1999; 99WO-US028551.

PR 16-DEC-1999; 99WO-US030095.

PR 05-JAN-2000; 2000WO-US000219.

PR 06-JAN-2000; 2000WO-US000376.

PR 11-FEB-2000; 2000WO-US003565.

PR 18-FEB-2000; 2000WO-US004342.

PR 24-FEB-2000; 2000WO-US005004.

PR 02-MAR-2000; 2000WO-US005841.

PR 15-MAR-2000; 2000WO-US006884.

PR 17-MAY-2000; 2000WO-US013705.

PR 22-MAY-2000; 2000WO-US014042.

PR 30-MAY-2000; 2000WO-US014941.

PR 02-JUN-2000; 2000WO-US015264.

PR 23-AUG-2000; 2000WO-US023522.  
PR 24-AUG-2000; 2000WO-US023328.  
PR 08-NOV-2000; 2000WO-US030952.  
PR 10-NOV-2000; 2000WO-US030873.  
PR 01-DEC-2000; 2000WO-US032678.  
PR 28-FEB-2001; 2001WO-US006520.  
PR 01-MAR-2001; 2001WO-US006666.  
PR 01-JUN-2001; 2001WO-US017800.  
PR 20-JUN-2001; 2001WO-US019692.  
PR 29-JUN-2001; 2001WO-US021066.  
PR 09-JUL-2001; 2001WO-US021735.  
PR 04-SEP-2001; 2001US-00946374.

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PA (GETH ) GENENTECH INC.

XX

PI Baker KP, Botstein D, Desnoyers L, Eaton DL, Ferrara N, Fong S;  
PI Gao W, Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;  
PI Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D, Watanabe CK;  
PI Williams PM, Wood WI;

XX

DR WPI; 2003-755122/71.

DR N-PSDB; ADD39873.

XX

PT New secreted and transmembrane PRO polypeptides useful for treating  
PT cancers, kidney disorders, Crohn's disease, diabetes mellitus, hyper- or  
PT hypo-insulinemia, sports injuries and arthritis.

XX

PS Claim 12; SEQ ID NO 282; 557pp; English.

XX

CC The invention relates to an isolated PRO polypeptide (secreted or  
CC transmembrane protein) having at least 80% amino acid sequence identity  
CC to an amino acid sequence chosen from 123 fully defined sequences as  
CC given in the specification (including their extracellular domains either  
CC or without their associated signal peptides. Also include are the  
CC nucleotide (NA) sequences encoding PRO, a vector comprising the PRO NA, a  
CC host cell comprising the vector, producing PRO, a chimaeric molecule  
CC comprising PRO fused to a heterologous amino acid sequence, and an anti-  
CC PRO antibody. Pro is useful as molecular weight markers for protein  
CC electrophoresis and also for chromosome identification. PRO is also  
CC useful for tissue typing. PRO and PRO NA are useful as hybridisation  
CC probes for a cDNA library to isolate the full-length PRO cDNA. PRO NA is  
CC useful for generating transgenic animals or knock-out animals which are  
CC useful in development and screening useful reagents. PRO NA is also  
CC useful in gene therapy. PRO1244, PRO1286 and PRO1303 polypeptides are  
CC useful for treating cancerous tumours. PRO1250, PRO1418 and PRO1410  
CC polypeptides are useful for suppressing immune response. PRO1246  
CC polypeptide is useful for treating cardiac insufficiency disorders.  
CC PRO1246 polypeptide is also useful for treating tumours. PRO1246 and  
CC PRO1561 polypeptide are useful for stimulating calcium flux in human  
CC umbilical vein endothelial cells. PRO1265, PRO1250 and PRO1474  
CC polypeptides are useful for treating bone and/or cartilage disorders  
CC (e.g., arthritis) and wound healing. PRO1130, PRO1275 and PRO1418  
CC polypeptides are useful for treating diabetes in skeletal muscle cells  
CC and obesity. PRO1265, PRO1244 and PRO1382 polypeptides are useful for  
CC treating Berger disease or other nephropathies associated with Schonlein-  
CC Henoch purpura, coeliac disease, dermatitis, herpetiformis or Crohn's  
CC disease. PRO1478, PRO1265, PRO1412, PRO1279, PRO1304, PRO1306, PRO1418,

CC PRO1410 and PRO1575 are useful in treating thalassaemias. The present  
CC sequence represents a PRO protein of the invention.  
XX  
SQ Sequence 523 AA;

Query Match 100.0%; Score 2768; DB 7; Length 523;  
Best Local Similarity 100.0%; Pred. No. 6.3e-278;  
Matches 523; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db      1 MAGQRVLLLVGFLLPGVLLSEAAKILTISTVGGSHYLLMDRVSQILQDHGHNVTMLNHKR 60

Qy     61 GPFMPDFKKEEKSYQVISWLAPEDHQREFKKSFDFFLEETLGGRGKFENLLNVLEYLALQ 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 GPFMPDFKKEEKSYQVISWLAPEDHQREFKKSFDFFLEETLGGRGKFENLLNVLEYLALQ 120

Qy    121 CSHFLNRKDIMDSLKNENFDMVIVETFDYCPFLIAEKLGPVFVAILSTSFGSLEFGLPIP 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 CSHFLNRKDIMDSLKNENFDMVIVETFDYCPFLIAEKLGPVFVAILSTSFGSLEFGLPIP 180

Qy    181 LSYVPVFRSLLTDHMDFWGRVKNFLMFFSFCCRQQHMQSTFDNTIKEHFTGSRPVLSHL 240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 LSYVPVFRSLLTDHMDFWGRVKNFLMFFSFCCRQQHMQSTFDNTIKEHFTGSRPVLSHL 240

Qy    241 LLKAELWFINSDFAFDFARPLLNTVYVGGLMEKPIKPVPQDLENFIAKFGDSGFVLVTL 300
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 LLKAELWFINSDFAFDFARPLLNTVYVGGLMEKPIKPVPQDLENFIAKFGDSGFVLVTL 300

Qy    301 GSMVNTCQNPEIFKEMNNAFAHLPQGVIWKCQCSHWPKDVHLAANVKIVDWLPQSDLLAH 360
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 GSMVNTCQNPEIFKEMNNAFAHLPQGVIWKCQCSHWPKDVHLAANVKIVDWLPQSDLLAH 360

Qy    361 PSIRLFVTHGGQNSIMEAIQHGVPVMGIPLFGDQPENMVRVEAKKFGVSIQLKKLKAETL 420
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Db    361 PSIRLFVTHGGQNSIMEAIQHGVPVMGIPLFGDQPENMVRVEAKKFGVSIQLKKLKAETL 420

Qy    421 ALKMKQIMEDKRYKSAAVAASVILRSHPLSPTQRLVGWIDHVLQTGGATHLKPYPVQQPW 480
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 ALKMKQIMEDKRYKSAAVAASVILRSHPLSPTQRLVGWIDHVLQTGGATHLKPYPVQQPW 480

Qy    481 HEQYLFDFVFVFLGLTLGTLWLWLCGKLLGMAVWWLRGARKVKET 523
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Db    481 HEQYLFDFVFVFLGLTLGTLWLWLCGKLLGMAVWWLRGARKVKET 523
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RESULT 10

ADD70320

ID ADD70320 standard; protein; 523 AA.

XX

AC ADD70320;

XX

DT 15-JAN-2004 (first entry)

XX

DE Human secreted/transmembrane protein PRO1780.

XX

KW Human; secreted protein; transmembrane protein; PRO; tumour;

KW immune response; cardiac insufficiency disorder; calcium flux;  
KW umbilical vein endothelial cell; bone disorder; cartilage disorder;  
KW arthritis; wound healing; diabetes; skeletal muscle cells; obesity;  
KW Berger disease; nephropathy; Schonlein-Henoch purpura; coeliac disease;  
KW dermatitis; herpetiformis; Crohn's disease; thalassaemia.  
XX  
OS Homo sapiens.  
XX  
PN US2003054406-A1.  
XX  
PD 20-MAR-2003.  
XX  
PF 06-DEC-2001; 2001US-00006818.  
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PR 05-JAN-1999; 99WO-US000106.  
PR 16-APR-1999; 99US-0129674P.  
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PR 20-JUL-1999; 99US-0144758P.  
PR 26-JUL-1999; 99US-0145698P.  
PR 01-SEP-1999; 99WO-US020111.  
PR 15-SEP-1999; 99WO-US021194.  
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PR 16-DEC-1999; 99WO-US030095.  
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PR 22-MAY-2000; 2000WO-US014042.  
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PR 09-JUL-2001; 2001WO-US021735.  
 PR 04-SEP-2001; 2001US-00946374.  
 XX  
 PA (GETH ) GENENTECH INC.  
 XX  
 PI Baker KP, Botstein D, Desnoyers L, Eaton DL, Ferrara N, Fong S;  
 PI Gao W, Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;  
 PI Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D, Watanabe CK;  
 PI Williams PM, Wood WI;  
 XX  
 DR WPI; 2003-708344/67.  
 DR N-PSDB; ADD70319.  
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 PT Novel isolated PRO polypeptide useful for tissue typing, modulating  
 PT biological activity of cell, as molecular weight markers in protein  
 PT electrophoresis, for treating arthritis, tumor.  
 XX  
 PS Claim 12; SEQ ID NO 282; 549pp; English.  
 XX  
 CC The invention relates to an isolated PRO polypeptide (secreted or

Query Match 100.0%; Score 2768; DB 7; Length 523;  
 Best Local Similarity 100.0%; Pred. No. 6.3e-278;  
 Matches 523; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MAGQRVLLLVGFLLPGVLLSEAAKILTISTVGGSHYLLMDRVSQILQDHGHNVMTLNHKR	60
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Qy	121	CSHFLNRKDIMDSLKNENFDMVIVETFDYCPFLIAEKLKPFVAILSTSFGSLEFGLPIP	180
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Qy	181	LSYVPVFRSLLTDHMDFWGRVKNFLMFFSFCRRQQHMQSTFDNTIKEHFTEGSRPVLSHL	240
Db	181	LSYVPVFRSLLTDHMDFWGRVKNFLMFFSFCRRQQHMQSTFDNTIKEHFTEGSRPVLSHL	240
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Db	241	LLKAELWFINSDFAFDFARPLLNTVYVGGLMEKPIKPVPQDLENFIAKFGDSGFVLVTL	300
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Qy	361	PSIRLFVTHGGQNSIMEAIQHGVPVMGIPLFGDQPENMVRVEAKKFGVSIQLKKLKAETL	420
Db	361	PSIRLFVTHGGQNSIMEAIQHGVPVMGIPLFGDQPENMVRVEAKKFGVSIQLKKLKAETL	420
Qy	421	ALKMKQIMEDKRYKSAVAASVILRSHPLSPTQRLVGWIDHVLQTGGATHLKPYPVQQPW	480
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QY 481 HEQYLFDFVFVFLGLTLGLTWLWLCGKLLGMAVWVWLRGARKVKET 523  
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 Db 481 HEQYLFDFVFVFLGLTLGLTWLWLCGKLLGMAVWVWLRGARKVKET 523

ADD38441

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PR	17-SEP-1998;	98US-0100919P.
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PR 05-JAN-1999; 99WO-US000106.  
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PR 23-JUN-1999; 99US-0141037P.  
PR 20-JUL-1999; 99US-0144758P.  
PR 26-JUL-1999; 99US-0145698P.  
PR 01-SEP-1999; 99WO-US020111.  
PR 15-SEP-1999; 99WO-US021194.  
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PR 16-DEC-1999; 99WO-US030095.  
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PR 11-FEB-2000; 2000WO-US003565.  
PR 18-FEB-2000; 2000WO-US004342.  
PR 24-FEB-2000; 2000WO-US005004.  
PR 02-MAR-2000; 2000WO-US005841.

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PR 10-NOV-2000; 2000WO-US030873.  
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PR 01-MAR-2001; 2001WO-US006666.  
PR 01-JUN-2001; 2001WO-US017800.  
PR 20-JUN-2001; 2001WO-US019692.  
PR 29-JUN-2001; 2001WO-US021066.  
PR 09-JUL-2001; 2001WO-US021735.  
PR 04-SEP-2001; 2001US-00946374.

XX

PA (GETH ) GENENTECH INC.

XX

PI Baker KP, Botstein D, Desnoyers L, Eaton DL, Ferrara N, Fong S;  
PI Gao W, Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;  
PI Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D, Watanabe CK;  
PI Williams PM, Wood WI;

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DR WPI; 2003-787000/74.

DR N-PSDB; ADD38440.

XX

PT Novel isolated PRO polypeptide, useful for treating cancerous tumors,  
PT cardiac insufficiency disorders, wound healing, diabetes mellitus,  
PT thalassemias.

XX

PS Claim 12; SEQ ID NO 282; 556pp; English.

XX

CC The invention relates to an isolated PRO polypeptide (secreted or  
CC transmembrane protein) having at least 80% amino acid sequence identity

Query Match 100.0%; Score 2768; DB 7; Length 523;  
Best Local Similarity 100.0%; Pred. No. 6.3e-278;  
Matches 523; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MAGQRVLLLVGFLLPGVLLSEAAKILTISTVGGSHYLLMDRVSQILQDHGHNVTMLNHKR 60  
  
Qy 61 GPFMPDFKKEEKSYQVISWLAPEHDHOREFKKSFDFLEETLGGRGKFENLLNVLEYLALQ 120  
|  
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Qy 121 CSHFLNRKDIMDSLKNENFDMVIVETFDYCPFLIAEKLKGKPFVAILSTSFGSLEFGLPIP 180  
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Db 121 CSHFLNRKDIMDSLKNENFDMVIVETFDYCPFLIAEKLKGKPFVAILSTSFGSLEFGLPIP 180  
  
Qy 181 LSYVPVFRSLLTDHMDFWGRVKNFLMFFSFCRRQQHMQSTFDNTIKEHFTEGSRPVLSHL 240  
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Qy 241 LLKAELWFINSDFAFDFARPLLPTVYVGGIMEKPIKPVQDLENFIAKFGDSGFVLVTL 300  
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 Db 241 LLKAELWFINSDFAFDFARPLLPTVYVGGIMEKPIKPVQDLENFIAKFGDSGFVLVTL 300

Qy 301 GSMVNTCQNPEIFKEMNNAFAHLPGQVIWKCQCSHWPKDVHLAANVKIVDWLPQSDLLAH 360  
 |||  
 Db 301 GSMVNTCQNPEIFKEMNNAFAHLPGQVIWKCQCSHWPKDVHLAANVKIVDWLPQSDLLAH 360

Qy 361 PSIRLFVTHGGQNSIMEAIQHGVPMVGIPFLGQDPENMVRVEAKKFGVSIQLKKLKAETL 420  
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 Db 361 PSIRLFVTHGGQNSIMEAIQHGVPMVGIPFLGQDPENMVRVEAKKFGVSIQLKKLKAETL 420

Qy 421 ALKMKQIMEDKRYKSAAVAASVILRSHPLSPTQRLVGWIDHVLQTGGATHLKPYPVQQPW 480  
 |||  
 Db 421 ALKMKQIMEDKRYKSAAVAASVILRSHPLSPTQRLVGWIDHVLQTGGATHLKPYPVQQPW 480

Qy 481 HEQYLFDFVFLGLTLGLTLWLCGKLLGMAVWWLRGARKVKET 523  
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 Db 481 HEQYLFDFVFLGLTLGLTLWLCGKLLGMAVWWLRGARKVKET 523

RESULT 12

ADD39397

ID ADD39397 standard; protein; 523 AA.

XX

AC ADD39397;

XX

DT 15-JAN-2004 (first entry)

XX

DE Human secreted/transmembrane protein PRO1780.

XX

KW Human; secreted protein; transmembrane protein; PRO; tumour;

KW immune response; cardiac insufficiency disorder; calcium flux;

KW umbilical vein endothelial cell; bone disorder; cartilage disorder;

KW arthritis; wound healing; diabetes; skeletal muscle cells; obesity;

KW Berger disease; nephropathy; Schonlein-Henoch purpura; coeliac disease;

KW dermatitis; herpetiformis; Crohn's disease; thalassaemia.

XX

OS Homo sapiens.

XX

PN US2003096954-A1.

XX

PD 22-MAY-2003.

XX

PF 07-DEC-2001; 2001US-00011671.

XX

PR 01-SEP-1998; 98US-0098716P.

PR 01-SEP-1998; 98US-0098723P.

PR 01-SEP-1998; 98US-0098749P.

PR 01-SEP-1998; 98US-0098750P.

PR 02-SEP-1998; 98US-0098803P.

PR 02-SEP-1998; 98US-0098821P.

PR 02-SEP-1998; 98US-0098843P.

PR 09-SEP-1998; 98US-0099536P.

PR 09-SEP-1998; 98US-0099596P.

PR 09-SEP-1998; 98US-0099598P.

PR 09-SEP-1998; 98US-0099602P.

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PR	10-SEP-1998;	98US-0099741P.
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PR	10-SEP-1998;	98US-0099816P.
PR	15-SEP-1998;	98US-0100385P.
PR	15-SEP-1998;	98US-0100388P.
PR	15-SEP-1998;	98US-0100390P.
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PR	24-SEP-1998;	98US-0101916P.
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PR	01-OCT-1998;	98US-0102684P.
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PR	02-OCT-1998;	98US-0102965P.
PR	06-OCT-1998;	98US-0103258P.
PR	06-OCT-1998;	98US-0103449P.
PR	07-OCT-1998;	98US-0103314P.
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PR	07-OCT-1998;	98US-0103328P.
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PR	08-OCT-1998;	98US-0103679P.
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PR	14-OCT-1998;	98US-0104257P.
PR	20-OCT-1998;	98US-0104987P.
PR	20-OCT-1998;	98US-0105000P.
PR	20-OCT-1998;	98US-0105002P.
PR	21-OCT-1998;	98US-0105104P.
PR	22-OCT-1998;	98US-0105169P.
PR	22-OCT-1998;	98US-0105266P.
PR	26-OCT-1998;	98US-0105693P.
PR	26-OCT-1998;	98US-0105694P.
PR	27-OCT-1998;	98US-0105807P.
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PR	27-OCT-1998;	98US-0105882P.
PR	27-OCT-1998;	98US-0106062P.
PR	28-OCT-1998;	98US-0106023P.
PR	28-OCT-1998;	98US-0106029P.
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PR	28-OCT-1998;	98US-0106032P.
PR	28-OCT-1998;	98US-0106033P.
PR	28-OCT-1998;	98US-0106178P.
PR	29-OCT-1998;	98US-0106248P.
PR	29-OCT-1998;	98US-0106384P.
PR	29-OCT-1998;	98US-0108500P.
PR	30-OCT-1998;	98US-0106464P.
PR	03-NOV-1998;	98US-0106856P.
PR	03-NOV-1998;	98US-0106902P.
PR	03-NOV-1998;	98US-0106905P.
PR	03-NOV-1998;	98US-0106919P.
PR	03-NOV-1998;	98US-0106932P.
PR	03-NOV-1998;	98US-0106934P.
PR	10-NOV-1998;	98US-0107783P.
PR	17-NOV-1998;	98US-0108775P.
PR	17-NOV-1998;	98US-0108779P.
PR	17-NOV-1998;	98US-0108787P.
PR	17-NOV-1998;	98US-0108788P.
PR	17-NOV-1998;	98US-0108801P.
PR	17-NOV-1998;	98US-0108802P.
PR	17-NOV-1998;	98US-0108806P.
PR	17-NOV-1998;	98US-0108807P.
PR	17-NOV-1998;	98US-0108867P.
PR	17-NOV-1998;	98US-0108925P.
PR	18-NOV-1998;	98US-0108848P.
PR	18-NOV-1998;	98US-0108849P.
PR	18-NOV-1998;	98US-0108850P.
PR	18-NOV-1998;	98US-0108851P.
PR	18-NOV-1998;	98US-0108852P.
PR	18-NOV-1998;	98US-0108858P.
PR	18-NOV-1998;	98US-0108904P.
PR	22-DEC-1998;	98US-0113296P.
PR	30-DEC-1998;	98US-0114223P.



PR 05-JAN-1999; 99WO-US000106.  
PR 16-APR-1999; 99US-0129674P.  
PR 23-JUN-1999; 99US-0141037P.  
PR 20-JUL-1999; 99US-0144758P.  
PR 26-JUL-1999; 99US-0145698P.  
PR 01-SEP-1999; 99WO-US020111.  
PR 15-SEP-1999; 99WO-US021194.  
PR 29-OCT-1999; 99US-0162506P.  
PR 30-NOV-1999; 99WO-US028313.  
PR 02-DEC-1999; 99WO-US028551.  
PR 16-DEC-1999; 99WO-US030095.  
PR 05-JAN-2000; 2000WO-US000219.  
PR 06-JAN-2000; 2000WO-US000376.  
PR 11-FEB-2000; 2000WO-US003565.  
PR 18-FEB-2000; 2000WO-US004342.  
PR 24-FEB-2000; 2000WO-US005004.  
PR 02-MAR-2000; 2000WO-US005841.  
PR 15-MAR-2000; 2000WO-US006884.  
PR 17-MAY-2000; 2000WO-US013705.  
PR 22-MAY-2000; 2000WO-US014042.  
PR 30-MAY-2000; 2000WO-US014941.  
PR 02-JUN-2000; 2000WO-US015264.  
PR 23-AUG-2000; 2000WO-US023522.  
PR 24-AUG-2000; 2000WO-US023328.  
PR 08-NOV-2000; 2000WO-US030952.  
PR 10-NOV-2000; 2000WO-US030873.  
PR 01-DEC-2000; 2000WO-US032678.  
PR 28-FEB-2001; 2001WO-US006520.  
PR 01-MAR-2001; 2001WO-US006666.  
PR 01-JUN-2001; 2001WO-US017800.  
PR 20-JUN-2001; 2001WO-US019692.  
PR 29-JUN-2001; 2001WO-US021066.  
PR 09-JUL-2001; 2001WO-US021735.  
PR 04-SEP-2001; 2001US-00946374.

XX

PA (GETH ) GENENTECH INC.

XX

PI Baker KP, Botstein D, Desnoyers L, Eaton DL, Ferrara N, Fong S;  
PI Gao W, Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;  
PI Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D, Watanabe CK;  
PI Williams PM, Wood WI;

XX

DR WPI; 2003-786999/74.

DR N-PSDB; ADD39396.

XX

PT Novel isolated PRO polypeptide useful for tissue typing, modulating  
PT biological activity of cell, as molecular weight markers in protein  
PT electrophoresis, for treating arthritis, tumor.

XX

PS Claim 12; SEQ ID NO 282; 550pp; English.

XX

CC The invention relates to an isolated PRO polypeptide (secreted or

Query Match 100.0%; Score 2768; DB 7; Length 523;  
Best Local Similarity 100.0%; Pred. No. 6.3e-278;  
Matches 523; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MAGQRVLLLVGFLLPGVLLSEAAKILTISTVGGSHYLLMDRVSQILQDHGHNVTMLNHKR	60
Db	1	MAGQRVLLLVGFLLPGVLLSEAAKILTISTVGGSHYLLMDRVSQILQDHGHNVTMLNHKR	60
Qy	61	GPFMPDFKKEEKSYQVISWLAPEDHQREFKKSFDFFLEETLGGRGKFENLLNVLEYLALQ	120
Db	61	GPFMPDFKKEEKSYQVISWLAPEDHQREFKKSFDFFLEETLGGRGKFENLLNVLEYLALQ	120
Qy	121	CSHFLNRKDIMDSLKNENFDMVIVETFDYCPFLIAEKLGKPFVAILSTSFGSLEFGLPIP	180
Db	121	CSHFLNRKDIMDSLKNENFDMVIVETFDYCPFLIAEKLGKPFVAILSTSFGSLEFGLPIP	180
Qy	181	LSYVPVFRSLLTDHMDFWGRVKNFLMFFSFCRRQQHMQSTFDNTIKEHFTEGSRPVLSHL	240
Db	181	LSYVPVFRSLLTDHMDFWGRVKNFLMFFSFCRRQQHMQSTFDNTIKEHFTEGSRPVLSHL	240
Qy	241	LLKAELWFINSDFAFDFARPLLNTVYVGGLMEKPIKPVPQDLENFIAKFGDSGFVLVTL	300
Db	241	LLKAELWFINSDFAFDFARPLLNTVYVGGLMEKPIKPVPQDLENFIAKFGDSGFVLVTL	300
Qy	301	GSMVNTCQNPEIFKEMNNAFAHLPPQGVWKCQCSHWPKDVHLAANVKIVDWLPQSDLLAH	360
Db	301	GSMVNTCQNPEIFKEMNNAFAHLPPQGVWKCQCSHWPKDVHLAANVKIVDWLPQSDLLAH	360
Qy	361	PSIRLFVTHGGQNSIMEAIQHGVPMVGIPFLFGDQPENMVRVEAKKFGVSIQLKKLKAETL	420
Db	361	PSIRLFVTHGGQNSIMEAIQHGVPMVGIPFLFGDQPENMVRVEAKKFGVSIQLKKLKAETL	420
Qy	421	ALKMKQIMEDKRYKSAAVAASVILRSHPLSPTQRLVGWIDHVLQTGGATHLKPYPVQQPW	480
Db	421	ALKMKQIMEDKRYKSAAVAASVILRSHPLSPTQRLVGWIDHVLQTGGATHLKPYPVQQPW	480
Qy	481	HEQYLFDFVFVFLGLTLGTLWLWLCGKLLGMAVWWLRGARKVKET	523
Db	481	HEQYLFDFVFVFLGLTLGTLWLWLCGKLLGMAVWWLRGARKVKET	523

# RESULT 13

ADD38920

ID ADD38920 standard; protein; 523 AA.

XX

AC ADD38920;

XX

DT 15-JAN-2004 (first entry)

XX

DE Human secreted/transmembrane protein PRO1780.

XX

KW Human; secreted protein; transmembrane protein; PRO; tumour;

KW immune response; cardiac insufficiency disorder; calcium flux;

KW umbilical vein endothelial cell; bone disorder; cartilage disorder;

KW arthritis; wound healing; diabetes; skeletal muscle cells; obesity;

KW Berger disease; nephropathy; Schonlein-Henoch purpura; coeliac disease;

KW dermatitis; herpetiformis; Crohn's disease; thalassaemia.

XX

OS Homo sapiens.

XX

PN US2003092061-A1.

XX  
PD 15-MAY-2003.  
XX  
PF 06-DEC-2001; 2001US-00007194.  
XX  
PR 01-SEP-1998; 98US-0098716P.  
PR 01-SEP-1998; 98US-0098723P.  
PR 01-SEP-1998; 98US-0098749P.  
PR 01-SEP-1998; 98US-0098750P.  
PR 02-SEP-1998; 98US-0098803P.  
PR 02-SEP-1998; 98US-0098821P.  
PR 02-SEP-1998; 98US-0098843P.  
PR 09-SEP-1998; 98US-0099536P.  
PR 09-SEP-1998; 98US-0099596P.  
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PR 09-SEP-1998; 98US-0099602P.  
PR 09-SEP-1998; 98US-0099642P.  
PR 10-SEP-1998; 98US-0099741P.  
PR 10-SEP-1998; 98US-0099754P.  
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PR 15-SEP-1998; 98US-0100388P.  
PR 15-SEP-1998; 98US-0100390P.  
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PR	07-OCT-1998;	98US-0103328P.
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PR	20-OCT-1998;	98US-0104987P.
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PR	22-OCT-1998;	98US-0105169P.
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PR	27-OCT-1998;	98US-0105881P.
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PR	03-NOV-1998;	98US-0106856P.
PR	03-NOV-1998;	98US-0106902P.
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PR	03-NOV-1998;	98US-0106934P.
PR	10-NOV-1998;	98US-0107783P.
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PR	17-NOV-1998;	98US-0108787P.

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PR 17-NOV-1998; 98US-0108802P.  
PR 17-NOV-1998; 98US-0108806P.  
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PR 18-NOV-1998; 98US-0108849P.  
PR 18-NOV-1998; 98US-0108850P.  
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PR 18-NOV-1998; 98US-0108852P.  
PR 18-NOV-1998; 98US-0108858P.  
PR 18-NOV-1998; 98US-0108904P.  
PR 22-DEC-1998; 98US-0113296P.  
PR 30-DEC-1998; 98US-0114223P.  
PR 05-JAN-1999; 99WO-US000106.  
PR 16-APR-1999; 99US-0129674P.  
PR 23-JUN-1999; 99US-0141037P.  
PR 20-JUL-1999; 99US-0144758P.  
PR 26-JUL-1999; 99US-0145698P.  
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PR 15-SEP-1999; 99WO-US021194.  
PR 29-OCT-1999; 99US-0162506P.  
PR 30-NOV-1999; 99WO-US028313.  
PR 02-DEC-1999; 99WO-US028551.  
PR 16-DEC-1999; 99WO-US030095.  
PR 05-JAN-2000; 2000WO-US000219.  
PR 06-JAN-2000; 2000WO-US000376.  
PR 11-FEB-2000; 2000WO-US003565.  
PR 18-FEB-2000; 2000WO-US004342.  
PR 24-FEB-2000; 2000WO-US005004.  
PR 02-MAR-2000; 2000WO-US005841.  
PR 15-MAR-2000; 2000WO-US006884.  
PR 17-MAY-2000; 2000WO-US013705.  
PR 22-MAY-2000; 2000WO-US014042.  
PR 30-MAY-2000; 2000WO-US014941.  
PR 02-JUN-2000; 2000WO-US015264.  
PR 23-AUG-2000; 2000WO-US023522.  
PR 24-AUG-2000; 2000WO-US023328.  
PR 08-NOV-2000; 2000WO-US030952.  
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PR 01-DEC-2000; 2000WO-US032678.  
PR 28-FEB-2001; 2001WO-US006520.  
PR 01-MAR-2001; 2001WO-US006666.  
PR 01-JUN-2001; 2001WO-US017800.  
PR 20-JUN-2001; 2001WO-US019692.  
PR 29-JUN-2001; 2001WO-US021066.  
PR 09-JUL-2001; 2001WO-US021735.  
PR 04-SEP-2001; 2001US-00946374.

XX

PA (GETH ) GENENTECH INC.

XX

PI Baker KP, Botstein D, Desnoyers L, Eaton DL, Ferrara N, Fong S;  
PI Gao W, Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;  
PI Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D, Watanabe CK;  
PI Williams PM, Wood WI;



AC ADD40351;  
 XX  
 DT 15-JAN-2004 (first entry)  
 XX  
 DE Human secreted/transmembrane protein PRO1780.  
 XX  
 KW Human; secreted protein; transmembrane protein; PRO; tumour;  
 KW immune response; cardiac insufficiency disorder; calcium flux;  
 KW umbilical vein endothelial cell; bone disorder; cartilage disorder;  
 KW arthritis; wound healing; diabetes; skeletal muscle cells; obesity;  
 KW Berger disease; nephropathy; Schonlein-Henoch purpura; coeliac disease;  
 KW dermatitis; herpetiformis; Crohn's disease; thalassaemia.  
 XX  
 OS Homo sapiens.  
 XX  
 PN US2003082627-A1.  
 XX  
 PD 01-MAY-2003.  
 XX  
 PF 06-DEC-2001; 2001US-00006117.  
 XX  
 PR 01-SEP-1998; 98US-0098716P.  
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PR 05-JAN-1999; 99WO-US000106.  
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PR 15-SEP-1999; 99WO-US021194.  
PR 29-OCT-1999; 99US-0162506P.  
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PR 17-MAY-2000; 2000WO-US013705.  
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PR 30-MAY-2000; 2000WO-US014941.  
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PR 23-AUG-2000; 2000WO-US023522.  
PR 24-AUG-2000; 2000WO-US023328.  
PR 08-NOV-2000; 2000WO-US030952.

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PR    01-JUN-2001; 2001WO-US017800.
PR    20-JUN-2001; 2001WO-US019692.
PR    29-JUN-2001; 2001WO-US021066.
PR    09-JUL-2001; 2001WO-US021735.
PR    04-SEP-2001; 2001US-00946374.
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PA (GETH ) GENENTECH INC.

PT

PI Baker KP, Botstein D, Desnoyers I, Eaton DL, Ferrara N, Fong S;  
PI Gao W, Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;  
PI Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D, Watanabe CK;  
PI Williams PM, Wood WI;

DR WPI; 2003-755104/71.

DR N-PSDB; ADD40350.

PT New isolated PRO polypeptides such as PRO1560, PRO444, PRO1018, PRO1773,  
PT PRO1244, PRO1246, are useful for treating cancerous tumors and cardiac  
PT insufficiency disorders.

PS Claim 12; SEQ ID NO 282; 550pp; English.

CC The invention relates to an isolated PRO polypeptide (secreted or

Query Match 100.0%; Score 2768; DB 7; Length 523;  
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Matches 523; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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ID ADE50572 standard; protein; 523 AA.

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AC ADE50572;

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DT 29-JAN-2004 (first entry)

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DE Human secreted/transmembrane protein PRO1780.

XX

KW Human; secreted protein; transmembrane protein; PRO; tumour;

KW immune response; cardiac insufficiency disorder; calcium flux;

KW umbilical vein endothelial cell; bone disorder; cartilage disorder;

KW arthritis; wound healing; diabetes; skeletal muscle cells; obesity;

KW Berger disease; nephropathy; Schonlein-Henoch purpura; coeliac disease;

KW dermatitis; herpetiformis; Crohn's disease; thalassaemia.

XX

OS Homo sapiens.

XX

PN US2003069179-A1.

XX

PD 10-APR-2003.

XX

PF 11-DEC-2001; 2001US-00015393.

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PR      10-NOV-2000; 2000WO-US030873.
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PR      28-FEB-2001; 2001WO-US006520.
PR      01-MAR-2001; 2001WO-US006666.
PR      01-JUN-2001; 2001WO-US017800.
PR      20-JUN-2001; 2001WO-US019692.
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PR      09-JUL-2001; 2001WO-US021735.
PR      04-SEP-2001; 2001US-00946374.

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PA (GETH ) GENENTECH INC.

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PI Baker KP, Botstein D, Desnoyers L, Eaton DL, Ferrara N, Fong S;  
PI Gao W, Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;  
PI Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D, Watanabe CK;  
PI Williams PM, Wood WI;

XX

DR WPI; 2003-708395/67.

DR N-PSDB; ADE50571.

XX

PT Novel secreted and transmembrane PRO polypeptides useful in the  
PT preparation of a medicament for treating a condition responsive to PRO  
PT polypeptide and as therapeutic agents e.g. vaccines.

XX

PS Claim 12; SEO ID NO 282; 555pp; English.

XX

CC The invention relates to an isolated PRO polypeptide (secreted or

Query Match 100.0%; Score 2768; DB 7; Length 523;  
Best Local Similarity 100.0%; Pred. No. 6.3e-278;  
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Qy	121	CSHFLNRKDIMDSLKNENFDMVIVETFDYCPFLIAEKLGKPFVAILSTS	SFGSLEFGLPIP	180

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Qy	301	GSMVNTCQNPEIFKEMNNAFAHLPQGVWKCQC SHWPKDVHLAANVKIVDWLPQSDLLAH	360
Db	301	GSMVNTCQNPEIFKEMNNAFAHLPQGVWKCQC SHWPKDVHLAANVKIVDWLPQSDLLAH	360
Qy	361	PSIRLFVTHGGQNSIMEAIQHGVPMVGIP LFGDQPENMVRVEAKKFGVSIQLKKLKAETL	420
Db	361	PSIRLFVTHGGQNSIMEAIQHGVPMVGIP LFGDQPENMVRVEAKKFGVSIQLKKLKAETL	420
Qy	421	ALKMKQIMEDKRYKSAAVAASVILRSHPLSPTQRLVGWIDHVLQTGGATHLKPYPVFQQPW	480
Db	421	ALKMKQIMEDKRYKSAAVAASVILRSHPLSPTQRLVGWIDHVLQTGGATHLKPYPVFQQPW	480
Qy	481	HEQYLFDFVFVFLGLTLGTLWLWLCGKLLGMAVWWLRGARKVKET	523
Db	481	HEQYLFDFVFVFLGLTLGTLWLWLCGKLLGMAVWWLRGARKVKET	523

Search completed: May 7, 2004, 17:31:21  
 Job time : 62 secs

OM protein - protein search, using sw model

Run on: May 7, 2004, 17:30:14 ; Search time 22 Seconds  
(without alignments)  
1227.290 Million cell updates/sec

Title: US-10-017-867A-282  
Perfect score: 2768  
Sequence: 1 MAGQRVLLLVGFLLPGVLLS.....GKLLGMAVWWLRGARKVKET 523

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued\_Patents\_AA:\*  
1: /cgn2\_6/ptodata/2/iaa/5A\_COMB.pep:\*  
2: /cgn2\_6/ptodata/2/iaa/5B\_COMB.pep:\*  
3: /cgn2\_6/ptodata/2/iaa/6A\_COMB.pep:\*  
4: /cgn2\_6/ptodata/2/iaa/6B\_COMB.pep:\*  
5: /cgn2\_6/ptodata/2/iaa/PCTUS\_COMB.pep:\*  
6: /cgn2\_6/ptodata/2/iaa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query			ID	Description
		Match	Length	DB		
1	674	24.3	533	5	PCT-US92-00282-3	Sequence 3, Appli
2	661.5	23.9	528	4	US-09-356-806-8	Sequence 8, Appli
3	658	23.8	531	5	PCT-US92-00282-6	Sequence 6, Appli
4	657	23.7	530	3	US-09-180-852-2	Sequence 2, Appli
5	651.5	23.5	524	4	US-09-356-806-40	Sequence 40, Appl
6	649	23.4	530	4	US-09-356-806-113	Sequence 113, App
7	629	22.7	531	5	PCT-US92-00282-5	Sequence 5, Appli
8	606	21.9	534	5	PCT-US92-00282-4	Sequence 4, Appli
9	600	21.7	529	5	PCT-US92-00282-7	Sequence 7, Appli
10	521	18.8	454	4	US-09-813-918-2	Sequence 2, Appli
11	503.5	18.2	288	4	US-09-813-918-3	Sequence 3, Appli



12	380	13.7	245	4	US-09-305-856B-18	Sequence 18, Appl
13	346.5	12.5	515	3	US-08-942-012B-32	Sequence 32, Appl
14	342.5	12.4	460	3	US-08-942-012B-33	Sequence 33, Appl
15	321	11.6	515	3	US-08-942-012B-24	Sequence 24, Appl
16	316.5	11.4	488	3	US-08-942-012B-29	Sequence 29, Appl
17	316.5	11.4	488	3	US-08-942-012B-30	Sequence 30, Appl
18	300	10.8	288	4	US-09-305-856B-2	Sequence 2, Appli
19	300	10.8	288	5	PCT-US92-00282-19	Sequence 19, Appl
20	272	9.8	493	3	US-08-942-012B-28	Sequence 28, Appl
21	259.5	9.4	489	3	US-08-942-012B-31	Sequence 31, Appl
22	258.5	9.3	287	4	US-09-305-856B-10	Sequence 10, Appl
23	256	9.2	310	4	US-09-305-856B-14	Sequence 14, Appl
24	255	9.2	289	4	US-09-305-856B-8	Sequence 8, Appli
25	252	9.1	286	5	PCT-US92-00282-9	Sequence 9, Appli
26	249	9.0	289	5	PCT-US92-00282-11	Sequence 11, Appl
27	248	9.0	506	3	US-08-942-012B-26	Sequence 26, Appl
28	246.5	8.9	506	3	US-08-942-012B-25	Sequence 25, Appl
29	246.5	8.9	506	6	5180581-2	Patent No. 5180581
30	244.5	8.8	289	4	US-09-305-856B-4	Sequence 4, Appli
31	244.5	8.8	289	5	PCT-US92-00282-15	Sequence 15, Appl
32	242	8.7	491	3	US-08-942-012B-27	Sequence 27, Appl
33	239	8.6	129	4	US-09-370-838-36	Sequence 36, Appl
34	227	8.2	317	4	US-09-305-856B-12	Sequence 12, Appl
35	226	8.2	289	4	US-09-305-856B-6	Sequence 6, Appli
36	226	8.2	289	5	PCT-US92-00282-13	Sequence 13, Appl
37	223	8.1	253	4	US-09-305-856B-16	Sequence 16, Appl
38	214	7.7	52	2	US-08-466-583-7	Sequence 7, Appli
39	214	7.7	52	4	US-08-265-427-7	Sequence 7, Appli
40	214	7.7	52	5	PCT-US95-07820-7	Sequence 7, Appli
41	202	7.3	58	2	US-08-466-583-9	Sequence 9, Appli
42	202	7.3	58	4	US-08-265-427-9	Sequence 9, Appli
43	202	7.3	58	5	PCT-US95-07820-9	Sequence 9, Appli
44	176	6.4	463	4	US-08-311-731A-7	Sequence 7, Appli
45	175	6.3	56	2	US-08-466-583-4	Sequence 4, Appli

#### ALIGNMENTS

##### RESULT 1

PCT-US92-00282-3

; Sequence 3, Application PC/TUS9200282

; GENERAL INFORMATION:

; APPLICANT: OWENS, IDA S.

; APPLICANT: RITTER, JOSEPH K.

; TITLE OF INVENTION: THE GENETIC LOCUS UGT1 AND A MUTATION

; TITLE OF INVENTION: THEREIN.

; NUMBER OF SEQUENCES: 40

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: CUSHMAN DARBY & CUSHMAN

; STREET: 1615 L STREET, N.W.

; CITY: WASHINGTON

; STATE: D.C.

; COUNTRY: U.S.A.

; ZIP: 20036-5601

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

```

;   COMPUTER:  IBM PC compatible
;   OPERATING SYSTEM:  PC-DOS/MS-DOS
;   SOFTWARE:  PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER:  PCT/US92/00282
;   FILING DATE:  19920110
;   CLASSIFICATION:  435
;   ATTORNEY/AGENT INFORMATION:
;   NAME:  SCOTT, WATSON T.
;   REGISTRATION NUMBER:  26581
;   REFERENCE/DOCKET NUMBER:  91532-PCT
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE:  202-861-3000
;   TELEFAX:  202-822-0944
;   TELEX:  6714627 CUSH
;   INFORMATION FOR SEQ ID NO:  3:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH:  533 amino acids
;   TYPE:  AMINO ACID
;   STRANDEDNESS:  single
;   TOPOLOGY:  linear
;   MOLECULE TYPE:  protein
PCT-US92-00282-3

```

```

Query Match          24.3%;  Score 674;  DB 5;  Length 533;
Best Local Similarity 33.8%;  Pred. No. 5.9e-63;
Matches 175;  Conservative 92;  Mismatches 212;  Indels 38;  Gaps 13;

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Qy      8 LLVGFL--PGVLLSEAAKILTISTVGGSHYLLMDRVSQILQDHGHNVTMLNHKRGPFMP 65
|::| || |::| |||| | |||:| | || || : :| |
Db     11 LVLGLLLCVLGPVVS HAGKILLI-PVDGSHWLSMLGAIQQ LQQRGHEIVVL-----AP 62

Qy     66 D---FKKEEKSYQVISWLAPEDHQRE-FKKSF-----DFFLEETLGGRGKFENLL 111
| : : : | : : : | ||| |:| | ||: : : :
Db     63 DASLYIRDGA FYTLKTY--PVPFQREDVKESFVSLGHN VFENDSFLQRVI---KTYKKIK 117

Qy    112 NVLEYLALQCSHFLNRKDIMDSLKNENFDMVIVETFDYCPFLIAEKL GKPFVAILSTSFG 171
| ||| |: |:|: || :|::: : | | : |: | | |
Db    118 KDSAMLLSGCSHLLHNKELMASLAESSFDVMLTDPFLPCSPIVAQYLSLPTVFFLHALPC 177

Qy    172 SLEF---GLPIPLSYVPVFRSLLTDHMDFWGRVKNFLMFFSFCRRQQHMQSTFDNTIKEH 228
|||| | | ||| | :||| | ||| |: | : | : |
Db    178 SLEFEATQCPNPF SYVPRPLSSHSDHMTFLQRVKNM LIAFSQNFLCDVVYSPY-ATLASE 236

Qy    229 FTEGSRPVLSHLLLKAELWFINSDFAFDFARPLLNTVYVGGLMEKPIKPVPQDLENFIA 288
| : : : || | :| ||| |: |:|: || |:|: | : |: | :|
Db    237 FLQ-REVTVQDLLSSASVWLFRSDFVKDYPRPIMPNMV FVGGINCLHQNPLSQEF EAYIN 295

Qy    289 KFGDSGFVLVTLGSMVNTCQNPEIFKEMNNAFAHL PQGVIWKCQC SHWPKDVHLAANVKI 348
| : | |: :| |||: : : :| || |:|: : : :| | :
Db    296 ASGEHGIVVFSLGSMVSEIPEKKAM-AIADALGKNPQT V LWRYTGT---RPSNLANNTIL 351

Qy    349 VDWL PQSDLLAHP SIRLFVTHGGQNSIMEAIQHGVPMVG I PLFGDQPENMVRVEAKKFGV 408
| |||:| || | |:| | : : |:| :| ||| :| ||| :| |:| | ||
Db    352 VKWLPQNDLLGHPMTRAFITHAGSHGVYESICNGVPMVM MP LFGDQMDNAKRMETKGAGV 411

Qy    409 SIQLKKLKAETLALKMKQIMEDKRYKSAAVAASVILRSHPLSPTQRLVGWIDHVLQTGGA 468

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      :: : :: :| | :| :: || || : | : : | : | | | : | : | ||
Db      412 TLNVLEMTSEDLENALKAVINDKSYKENIMRLSSLHKDRPVEPLDLAVFWVEFVMRHKGA 471

Qy      469 THLKPYVFQQPWHEQYLFDFVFVLLGLTLGLTLWLCGK 505
      ||:| | : : || ||| : | : : |
Db      472 PHLRPAAHDLTWYQYHSLDVIGFLLAVVLTVAFITFK 508

```

RESULT 2

```

US-09-356-806-8
; Sequence 8, Application US/09356806
; Patent No. 6586175
; GENERAL INFORMATION:
; APPLICANT: Penny, Laura
; APPLICANT: Galvin, Margaret
; APPLICANT: Miller, Andrew
; APPLICANT: Reidy, Michael
; TITLE OF INVENTION: Genotyping Human
; TITLE OF INVENTION: UDP-Glucuronosyltransferase 2B4 (UGT2B4), 2B7 (UGT2B7)
and
; TITLE OF INVENTION: 2B15 (UGT2B15) Genes
; FILE REFERENCE: SEQ-22PRV2
; CURRENT APPLICATION NUMBER: US/09/356,806
; CURRENT FILING DATE: 1999-07-20
; NUMBER OF SEQ ID NOS: 164
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 8
; LENGTH: 528
; TYPE: PRT
; ORGANISM: H. sapiens
US-09-356-806-8

```

```

Query Match          23.9%; Score 661.5; DB 4; Length 528;
Best Local Similarity 34.2%; Pred. No. 1.3e-61;
Matches 173; Conservative 87; Mismatches 215; Indels 31; Gaps 15;

```

```

Qy      34 SHYLLMDRVSQILQDHGHNVTMLNHKRG----PFMPDFKKEEKSYQVISWLAPEDHQREF 89
      ||:: : : | || ||:| | | | : : || ::
Db      34 SHWMNIKTILDELVQRGHEVTVLASSASISFDPNSTLKFVYVPVSLTKTEFEDIKQL 93

Qy      90 KKSFDFFLEETLGGRGKFENLLNVL----EYLAQCShFLNRKDIMDSLKNENFDMVIVE 145
      | : ::| | : :: : | | :: | : | | : ||:| : :
Db      94 VKRWAELPKDTFW--SYFSQVQEIMWTFNDILRKFCCKDIVSNKKLMKKLQESRFDVVILAD 151

Qy      146 TFDYCPF--LIAEKLGPFPVAILSTSFG--SLE---FGLPIPLSYVPVFRSLTLDHMDFWG 199
      || |::| | || | | | :| || | |||| | | :| | |
Db      152 A--VFPFGELLAELLKIPFVYSLRFSPGYAIEKHSGGLLFPPSYVPVVMSELSDQMTFIE 209

Qy      200 RVKN--FLMFFSFCRRQOHMQSTFDNTIKEHFTGSRPVLSHLLLKAELWFINSDFAFDF 257
      |||| ::::| | : | : : | | | : ||:| | : : | |
Db      210 RVKNMIYVLYFEFWFQIFDMKK--WDQFYSE--VLGRPTTLSETMAKADIWLIRNYWDFQF 266

Qy      258 ARPLLNPNTVYVGGLMEKPIKPVPQDLENFIAKFGDSGFVLVTLGSMV-NTCQNPEIFKEM 316
      ||||| :||| || ||:|:::| | : |::| | : :||| || : | :
Db      267 PHPLLNPVFEFVGGLHCKPAKPLPKEMEETFQSSGENGVVVFSLGSMVSNSTSE--ERANVI 324

Qy      317 NNAFAHLPOGVIWKCQCSHWPKDVHLAANVKIVDWLPQSDLLAHPsirLFVTHGGQNSIM 376

```

```

      :| | :|| |:| : | | | :| :||:|||| | | | |:|||| | |
Db      325 ASALAKIPQKVLWRF DGN---KPD T LGLNTRLYKWIPQNDLLGHPKTRAFITHGGANGIY 381

Qy      377 EAIQHGVPMVGIPLEFGDQPENMVRVEAKKFGVSIQLKKLKAETLALKMKQIMEDKRYKSA 436
      ||| ||:||||:|||| |||:|: :|| | |: : : | :| :| | ||
Db      382 EAIYHGIPMVGVP LFADQPDNIAHMKAKGA AVSLDFHTMSSTDLLNALKTVINDPLYKEN 441

Qy      437 AVAASVILRSHPLSPTQRLVGWIDHVLQTGGATHLKPYVFQQPWHEQYLFDFVFLLGLT 496
      |: | | |: | | ||: |:| || |: | : : || |||
Db      442 AMKLSRIHHDQPVKPLDRAVFWIEFVMRHKGAKHLRVA AHDLTW FQYHSLDVTGFL LACV 501

Qy      497 LGTLWL CGKLLGMAVW-WLRGARKVK 521
      ::: | | || :| :| |
Db      502 ATVIFIITKCL-FCVWKEFVRTGKKGK 526

```

RESULT 3

PCT-US92-00282-6

```

; Sequence 6, Application PC/TUS9200282
; GENERAL INFORMATION:
;   APPLICANT: OWENS, IDA S.
;   APPLICANT: RITTER, JOSEPH K.
;   TITLE OF INVENTION: THE GENETIC LOCUS UGT1 AND A MUTATION
;   TITLE OF INVENTION: THEREIN.
;   NUMBER OF SEQUENCES: 40
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: CUSHMAN DARBY & CUSHMAN
;     STREET: 1615 L STREET, N.W.
;     CITY: WASHINGTON
;     STATE: D.C.
;     COUNTRY: U.S.A.
;     ZIP: 20036-5601
; COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: PCT/US92/00282
;   FILING DATE: 19920110
;   CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
;   NAME: SCOTT, WATSON T.
;   REGISTRATION NUMBER: 26581
;   REFERENCE/DOCKET NUMBER: 91532-PCT
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 202-861-3000
;   TELEFAX: 202-822-0944
;   TELEX: 6714627 CUSH
; INFORMATION FOR SEQ ID NO: 6:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 531 amino acids
;     TYPE: AMINO ACID
;     STRANDEDNESS: single
;     TOPOLOGY: linear
;   MOLECULE TYPE: protein
PCT-US92-00282-6

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Query Match 23.8%; Score 658; DB 5; Length 531;  
 Best Local Similarity 30.9%; Pred. No. 3e-61;  
 Matches 171; Conservative 106; Mismatches 211; Indels 66; Gaps 17;

Qy	1	MAGQRVLLLVGFLLPGVLLSEAAKILTISTVGGSHYLLMDRVSQILQDHGHNVTMLNHKR	60
		:     :    :   :  : :    :      :      :	
Db	7	LRGLSGLLLLLLALP---WAEKGKVL-VFMEGSHWLSMRDVVRELHARGHQAVAL---	58
Qy	61	GPFPDFKKEEKSYQVISWLAP---EDHQREF---KKSFD-----FFLEETLGGRGK	106
		:     : : :   :         :	
Db	59	APEVTVMHKGEDFFTLQTYAFPTYKEEYQREILGNACKGFEPQHFVKTF--ETMASIKK	116
Qy	107	FENLLNVLEYLALQCSHFLNRKDIMDSLKNENFDMVIVETFDYCPFLIAEKLKPFVAIL	166
		:        :  :  :  :  :  :  :  :  :  :  :  :	
Db	117	FFDL-----YANSCAALLHNKTLIQQLNSSSFVVLTDVPVFCGALLAKYLQIPAVFFL	170
Qy	167	STSFGSLEF---GLPIPLSYVPVFRSLTLDHMDFWGRVKNFLMFFS---FCRRQOHMQST	220
		: : :       :  :  :            :     :	
Db	171	RSVPCGIDYEATQCPKPSSYIPNLLTMSLDHMTFLQRVKNMLYPLTLKYIC---HLSIT	226
Qy	221	FDNTIKEHFTEGSR---PVLSHLLLKAELWFINSDFAFDFARPLLNTVYVGGLMKPIK	277
		: : :         :    -  :   :      :	
Db	227	PYESLASELLQREMSLVEVLH----ASVWLFRGDFVFDYPRPIMPNMVFIGGINCVIKK	282
Qy	278	PVPQDLENFIAKFGDSGFVLVTLGSMVNTCQNPEIFKEMNNAFAHLPQGVWKCQCCHWP	337
		:   :   : :   :   : :       : :   :   :    : : : :	
Db	283	PLSQEFEAYVNASGEHGIVVFSLGSMVSEIPEKKAM-EIAEALGRIPQTLWRYTGT---	338
Qy	338	KDVHLAANVKIVDWLPQSDLLAHPsirLVTHGGQNSIMEAIQHGVPMVGIPLFGDQPEN	397
		: :      :       :        :      :     :      :       :	
Db	339	RPSNLAKNTILVKWLPQNDLLGHPKARAFITHSGSHGIYEGICNGVPMVMMPLEFGDQMDN	398
Qy	398	MVRVEAKKFGVSIQLKKLKAETLALKMKQIMEDKRYKSAAVAASVILRSHPLSPTQRLVG	457
		:  :   : : : :   :   :  : :      :   : :   :	
Db	399	AKRMETRGAGVTNLVLEMTADDLENALKTVINNKSYKENIMRLSSLHKDRPIEPLDLAVF	458
Qy	458	WIDHVLQTTGGATHLKPYVFQQPWHEQYLFDFVFLLGLTLGLTLWL-----CGKLLGM	509
		: :    :      :  : : :        :   : :	
Db	459	WVEYVMRHKGAPHLRPAHDLTWYQYHSLDVGFLLAIVLTVVFIVYKSCAYGCRKCFG-	517
Qy	510	AVWWLRGARKVKET	523
		:    : :	
Db	518	-----GKGRVKKS	525

RESULT 4

US-09-180-852-2

; Sequence 2, Application US/09180852

; Patent No. 6287834

; GENERAL INFORMATION:

; APPLICANT: BELANGER, Alain

; APPLICANT: HUM, Dean W.

; APPLICANT: BEAULIEU, Martin

; APPLICANT: LEVESQUE, Eric

; TITLE OF INVENTION: CHARACTERIZATION AND USE OF AN ISOLATED URIDINE

; TITLE OF INVENTION: DIPHOSPHO-GLUCURONOSYLTRANSFERASE

```
; FILE REFERENCE: 1259-449
; CURRENT APPLICATION NUMBER: US/09/180,852
; CURRENT FILING DATE: 1999-02-08
; EARLIER APPLICATION NUMBER: PCT/CA97/00328
; EARLIER FILING DATE: 1997-05-16
; EARLIER APPLICATION NUMBER: US 08/649,319
; EARLIER FILING DATE: 1996-05-17
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 530
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-180-852-2
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Query Match          23.7%; Score 657; DB 3; Length 530;
Best Local Similarity 32.6%; Pred. No. 3.9e-61;
Matches 159; Conservative 92; Mismatches 211; Indels 26; Gaps 11;
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Qy      34 SHYLLMDRVSQILQDHGHNVMTLNHKGPFMPDFKKEEKSYQVI-SWLAPEDHQREFKKS 92
      ||:: | : : | || | : | : | : | : | : |
Db      34 SHWINMKTILEELVQRGHEVIVLTSSASILVNASKSSAIKLEVYPTSLTKNDLEDFFMKM 93

Qy      93 FDFFLEETLGGRGKFENLLNVLEYLALQCSHF-----LNRKDIMDSLKNENFDMVI 143
      || : : | : : | : | : | : | : | : | : |
Db      94 FDRWTYSI--SKNTFWSYFSQLQELCWEYSDDYNIKLCEDAVLNKK-LMRKLQESKFDVLL 150

Qy     144 VETFDYCPFLIAEKLKGPFFVAILSTSFSG-SLE---FGLPIPLSYVPVFRSLTDMDFWG 199
      : : | |::| | ||: | | |::| | | | | | | | |
Db     151 ADAVNPCGELLAELLNIPFLYSLRFSVGYTVEKNGGGFLFPPSYVPVVMSELSQMI FME 210

Qy     200 RVKN--FLMFFSFCRRQQHMQSTFDNTIKEHFTEGSRPVLSHLLLKAELWFINSDFAFDF 257
      |::| ::::| | : : : | | | | : | | | : | | |
Db     211 RIKNMIYMLYDFDFWQAYDLKK-WDQFYSE--VLGRPTTLFETMGKAEMWLIRTYWDFEF 267

Qy     258 ARPLLPNTVYVGGIMEKPIKPVPQDLENFIAKFGDSGFVLVTLGSMVNTCQNPEIFKEMN 317
      || ||| :||| | |||:|::| | : |::| | : |::| : | :
Db     268 PRPFLPNVDFVGGHLCKPAKPLPKEMEEFVQSSGENGIVVFSLGSMISN-MSEESANMIA 326

Qy     318 NAFALPQGVWKQCQSHWPKDVHLAANVKIWDWLPQSDLLAHPSIRLFVTHGGQNSIME 377
      : | | :|| |::| | | | | : | |::| | | : |::| | | |
Db     327 SALAQIPQKVLWREFD---GKKPNTLGSNTRLYKWLPQNDLLGHPKTKAFITHGGTNGIYE 383

Qy     378 AIQHGVPMVGIPLEFGDQPENMVRVEAKKFGVSIQLKKLKAETLALKMKQIMEDKRYKSAA 437
      || ||:||||||| || :| :::| | ::: : : | : : : | ||
Db     384 AIYHGIPMVGIPLEADQHDNIAHMKAKGAALSVDIRTMSRDLLNALKSVINDPIYKENI 443

Qy     438 VAASVILRSHPLSPTQRLVGWIDHVLQTTGATHLKPYVFPQWPWHEQYLFDFVFLGLTL 497
      : | | | : | | ||: |:: | | ||: | : : | | ||
Db     444 MKLSRIHHDQPVKPLDRAVFWIEFVMRHKGAKHLRVAAHNLTWIIQYHSLDVIAFLLACVA 503

Qy     498 GTLWLCGK 505
      ::: |
Db     504 TMIFMITK 511
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RESULT 5

US-09-356-806-40  
; Sequence 40, Application US/09356806  
; Patent No. 6586175  
; GENERAL INFORMATION:  
; APPLICANT: Penny, Laura  
; APPLICANT: Galvin, Margaret  
; APPLICANT: Miller, Andrew  
; APPLICANT: Reidy, Michael  
; TITLE OF INVENTION: Genotyping Human  
; TITLE OF INVENTION: UDP-Glucuronosyltransferase 2B4 (UGT2B4), 2B7 (UGT2B7)  
and  
; TITLE OF INVENTION: 2B15 (UGT2B15) Genes  
; FILE REFERENCE: SEQ-22PRV2  
; CURRENT APPLICATION NUMBER: US/09/356,806  
; CURRENT FILING DATE: 1999-07-20  
; NUMBER OF SEQ ID NOS: 164  
; SOFTWARE: FastSEQ for Windows Version 3.0  
; SEQ ID NO 40  
; LENGTH: 524  
; TYPE: PRT  
; ORGANISM: H. sapiens  
US-09-356-806-40

Query Match 23.5%; Score 651.5; DB 4; Length 524;  
Best Local Similarity 31.5%; Pred. No. 1.5e-60;  
Matches 163; Conservative 87; Mismatches 212; Indels 55; Gaps 14;

Qy	34	SHYLLMDRVSQILQDHGHNVMTLNHKGKRG-PFMPD-----FKKEEKSQY---Q	75
		: : :         :     :     : :	
Db	34	SHWMNIKTILDELIQRGHEVTVLASSASILFDPNNSSALKIEIYPTSLTKTELENFIMQQ	93
Qy	76	VISWL-APEDHQREFKKSFDFFLEETLGGRGKFENLLNVLEYLALQ-CSHFLNRKDIMDS	133
		:     :   :   : : : : :   :	
Db	94	IKRWSDLPKD-----TFWLYFSQV-----QEIMSIFGDITRKFCKDVVSNNKFKMCK	139
Qy	134	LKNENFDMVIVETFDYCPFLIAEKLKGKPFVAILSTS-----FGSLEFGLPIPLSYVPVFRS	189
		: :     : :     :	
Db	140	VQESRFDVIFADAI FPCSELLAELFNIPFVYLSFSFGYTFEKHSGGFI FPPSYVPVVMMS	199
Qy	190	LLTDHMDFWGRVKN--FLMFFSFCRRQQHMQSTFDNTIKEHFTE---GSRPVLSHLLKA	244
		: : :       :       :	
Db	200	ELTDQMTFMERVKNMIYVLYFDF-----WFEIFDMKKWDQFYSEVLGRPTTLSETMGKA	253
Qy	245	ELWFINSDFAFDFARPLLNPNTVYVGGLMKPKIPVPQDLENFIAKFGDSGFVLTGSMV	304
		: :     : :           :           : :     : :	
Db	254	DVWLIRNSWNFQFPYPLLPNVDFVGGHLCKPAKPLPKEMEDFVQSSGENGVVVFSLGSMV	313
Qy	305	NTCQNPEIFKEMNNAFAHLPGQVWKQCQSHWPKDVHLLAANVKIVDWLPQSDLLAHPSIR	364
		:   : :     :     : :     :   :   :	
Db	314	SN-MTEERANVIASALAIQIPQKVLWRFDGN---KPDTLGLNTRLYKWIPQNDLLGHPKTR	369
Qy	365	LFVTHGGQNSIMEAIQHGVPVMGVIPLFGDQPENMVRVEAKKFGVSIQLKKLKAETLALKM	424
		:                             : : :   : :   :	
Db	370	AFITHGGANGIYEAIYHGIPMVGVIPLFADQPDNIAHMKARGAAVRVDFNTMSSTDLLNAL	429
Qy	425	KQIMEDKRYKSAAVAASVILRSHPLSPTQRLVGWIDHVLQTGGATHLKPYPVQQPWHEQY	484
		: :     :     :         : :       :   : :	





Db 328 ALAQIPQKVLWRFD---GKKPNTLGSNTRLYKWLPQNDLLGHPKTKAFITHGGTNGIYEA 384

Qy 379 IQHGVPMVGIPFGDQPENMVRVEAKKFGVSIQLKKLKAETLALKMKQIMEDKRYKSAAV 438  
| | : | | | | | | | | : | : : : : | : | : : | | :

Db 385 IYHGIPMVGIPFADQHDNIAHMKAKGAALSVDIRTMSSRDLLNALKSVINDPVYKENVM 444

Qy 439 AASVILRSHPLSPTQRLVGWIDHVLQTGGATHLKPYVFQQPWHEQYLFDFVFVLLGLTLG 498  
| | : | | | | : | : : | | | : | : : | | | |

Db 445 KLSRIHHDQPMKPLDRAVFWIEFVMRHKGAKHLRVAAHNLTWIIQYHSLDVIAFLLACVAT 504

Qy 499 TLWLCKG 505  
: : : |

Db 505 VIFIITK 511

RESULT 7

PCT-US92-00282-5

; Sequence 5, Application PC/TUS9200282

; GENERAL INFORMATION:

; APPLICANT: OWENS, IDA S.

; APPLICANT: RITTER, JOSEPH K.

; TITLE OF INVENTION: THE GENETIC LOCUS UGT1 AND A MUTATION

; TITLE OF INVENTION: THEREIN.

; NUMBER OF SEQUENCES: 40

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: CUSHMAN DARBY & CUSHMAN

; STREET: 1615 L STREET, N.W.

; CITY: WASHINGTON

; STATE: D.C.

; COUNTRY: U.S.A.

; ZIP: 20036-5601

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: PCT/US92/00282

; FILING DATE: 19920110

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: SCOTT, WATSON T.

; REGISTRATION NUMBER: 26581

; REFERENCE/DOCKET NUMBER: 91532-PCT

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 202-861-3000

; TELEFAX: 202-822-0944

; TELEX: 6714627 CUSH

; INFORMATION FOR SEQ ID NO: 5:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 531 amino acids

; TYPE: AMINO ACID

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: protein

PCT-US92-00282-5

Query Match 22.7%; Score 629; DB 5; Length 531;  
 Best Local Similarity 30.4%; Pred. No. 3.8e-58;  
 Matches 159; Conservative 100; Mismatches 218; Indels 46; Gaps 13;

```

Qy      4 QRVLLLVGFL-LPGVLLSEAAKILTISTVGGSHYLLMDRVSQILQDHGHNVTMLNHKRG 62
      ||:  | || | |:::  :  |:| :  ||:| |  : ::| | || : ::
Db      9 QRISAGVFFLALWGMVVG D--KLLVVPQ-DGSHWLSMKDIVEVLSDRGHEIVVV----- 59

Qy     63 EMPDFK---KEEKSYQVISWLAPEDHQREFKKSFDFFLEETLGGRG-----KFENLLN 112
      :|:  || | |  :  | | | | |  :  |  : :: | :
Db     60 -VPEVNLLLKEYKYYTRKIYPVPYD-QEELKNRYQSFGNNHFAERSFLTAPQTEYRNNMI 117

Qy    113 VLEYLALQCSHFLNRKDIMDSLKNENFDMVIVETFDYCPFLIAEKLKGPVFAILSTSFGS 172
      |:  : |  |  : | ::  |  || :  :  : || || | | :  |
Db    118 VIGLYFINCQSLQDRDTL NFFKESKFDALFTDPALPCGVILA EYLG LPSVYLFRGFPCS 177

Qy    173 LEFGL---PIPLSYVPVFRSLLTDHMDFWGRVKNFL-----MFFSFCRRQQHMQSTFD 222
      ||  | |::| |  :  : || | | | || | |  :|:  : : : |
Db    178 LEHTFSRSPDPVSYIPRCYTKFS DHMTFSQRVANFLVNLEPYLFYCLFSKYEKLASA-- 235

Qy    223 NTIKEHFTEGSRPVLSHLLLKAE LWFINSDFAFDFARPLL PNTVYVGGIMEKPIKPVPQD 282
      :|  | |  | :  : | :  || :: ||::|| |::||:  | | : |:
Db    236 -VLK-----RDVDIITLSEVSVWLLRYDFVLEYPRPVM PNMVFIGGINCKKRKDL SQE 287

Qy    283 LENFIAKFGDSGFVLVTLGSMVNTCQNPEIFKEMNNAFAHLPQGV IWKQCQSHWPKDVHL 342
      | :|  | : | | : | || | :  :  : |  || | :| :  : : |
Db    288 FEAYINASGEHGIVV FSLGSMVSEIPEKKAM-AIADALGKNPQTVLWRYTGT---RPSNL 343

Qy    343 AANVKIVDWLPQSDLLAHPSIRLFVTHGGQNSIMEAIQHGVPMVGIPLFGDQPENMVRVE 402
      | |  : | |||: || | | | : || | :  : | : | || | : | || | : | | : |
Db    344 ANNTILVKWLPQNDLLGHPMTRAFITHAGSHGVYESICNGVPMVMMPLEFGDQMDNAKRME 403

Qy    403 AKKFGVSIQLKKLKAETLALKMKQIMEDKRYKSAAVAASVILRSHPLSPTQRLVGWIDHV 462
      |  ||:: : : : | |  : | :: || ||  :  | : :  | : |  | |:: |
Db    404 TKGAGVTINVLEMTSEDLENALKAVINDKSYKENIMRLSSLHKDRPVEPLDLAVFWVEFV 463

Qy    463 LQTGGATHLKPYVFQQPWHEQYLFDFVFVFLGLTLGLTLWL CGK 505
      ::  || ||:|  |:: :  ||  ||| : |  ::  |
Db    464 MRHKGAPHLRPA AHDLTWYQYHSLDVIGFLLAVVLTVAFITFK 506
  
```

# RESULT 8

PCT-US92-00282-4

; Sequence 4, Application PC/TUS9200282

; GENERAL INFORMATION:

; APPLICANT: OWENS, IDA S.

; APPLICANT: RITTER, JOSEPH K.

; TITLE OF INVENTION: THE GENETIC LOCUS UGT1 AND A MUTATION

; TITLE OF INVENTION: THEREIN.

; NUMBER OF SEQUENCES: 40

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: CUSHMAN DARBY & CUSHMAN

; STREET: 1615 L STREET, N.W.

; CITY: WASHINGTON

; STATE: D.C.

; COUNTRY: U.S.A.

; ZIP: 20036-5601

```

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/00282
; FILING DATE: 19920110
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: SCOTT, WATSON T.
; REGISTRATION NUMBER: 26581
; REFERENCE/DOCKET NUMBER: 91532-PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-861-3000
; TELEFAX: 202-822-0944
; TELEX: 6714627 CUSH
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 534 amino acids
; TYPE: AMINO ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US92-00282-4

```

```

Query Match          21.9%; Score 606; DB 5; Length 534;
Best Local Similarity 31.3%; Pred. No. 1.1e-55;
Matches 163; Conservative 94; Mismatches 218; Indels 46; Gaps 13;

```

```

Qy      8 LLVGFLLPGVLLS-----EAAKILTISTVGGSHYLLMDRVSQILQDHGHNVTMLNHKRG 62
      | | || || | : | : | : | | : | | : | | : |
Db     12 LATGLLL---LLSVQPWAESGKVLVVPT-DGSPWLSMREALRELHARGHQAVVLT----P 63

Qy     63 FMPDFKKEEKSYQVISWLAPEDHQREFKKSFDFFLEETLG---GRGKFENLL----- 111
      : |||| : : : : | | : || : ||| | : | : ||
Db     64 EVNMHIKEEKFFTLTAYAVPWT-QKEFDR-----VTLGYTQGGFFETEHLKRYSRMA 115

Qy    112 ---NVLEYLALQCSHFLNRKDIMDSLKNENFDMVIVETFDYCPFLIAEKLKGPFAVAILST 168
      || | | | : : : : | : || : : : | : : | | |
Db    116 IMNNVSLALHRCCVELLHNEALIRHLNATSFDDVLTDPVNLCGAVLAKYLSIPAVFFWRY 175

Qy    169 SFGSLEF---GLPIPLSYVPVFRSLLTDHMDFWGRVKNFLMFFSFCRRQQHMQSTFDNTI 225
      | : | | | || : | : : ||| | ||| | : : :
Db    176 IPCDLDFKGTQCPNPSSYIPKLLTTNSDHMTFLQRVKNMLYPLALSYICHTFSAPYASIA 235

Qy    226 KEHFTEGSRPV-LSHLLLKAEIWFINSDFAFDFARPLLNTVYVGGGLMEKPIKVPQDLE 284
      | | | | : | : | : | | | : || : || : || : || : || : |
Db    236 SELF---QREVSVDLVSYASVWLFGRGDFVMDYPRPIMPNMVFIGGINCANGKPLSQEFE 292

Qy    285 NFIAKFGDSGFVLVTLGSMVNTCQNPEIFKEMNNAFAHLPPQGVWKCQCQSHWPKDVHLAA 344
      : | | : | : : |||| : : : : | : || | : : : : : ||
Db    293 AYINASGEHGIVVFSLGSMVSEIPEKKAM-AIADALGKIPQTVLWRYTGT---RPSNLAN 348

Qy    345 NVKIVDWLPQSDLLAHPsirLfvthggQNSIMEAIQHGVPMVGIPLFQDQPENMVRVEAK 404
      | : | ||| : || | | : || | : : | : ||| : |||| : | | : |
Db    349 NTILVKWLPQNDLLGHMPTRAFITHAGSHGVYESICNGVPMVMMPLEFGDQMDNAKRMETK 408

```

Qy 405 KFGVSIQLKKLKAETLALKMKQIMEDKRYKSAAVAASVILRSHPLSPTQRLVGWIDHVLQ 464  
 ||:: : :: :| | :| :: || || : | : : |: | | |:: |::  
 Db 409 GAGVTNLNLEMTSEDLENALKAVINDKSYKENIMRLSSLHKDRPVEPLDLAVFWVEFVMR 468  
 Qy 465 TGGATHLKPYVFQQPWHEQYLFDFVFVFLGLTLGLTLWLCLGK 505  
 || ||:| |:: : || ||| : | :: |  
 Db 469 HKGAPHLRPAAHDLTWYQYHSLDVIGFLLAVVLTVAFITFK 509

RESULT 9

PCT-US92-00282-7

; Sequence 7, Application PC/TUS9200282

; GENERAL INFORMATION:

; APPLICANT: OWENS, IDA S.

; APPLICANT: RITTER, JOSEPH K.

; TITLE OF INVENTION: THE GENETIC LOCUS UGT1 AND A MUTATION

; TITLE OF INVENTION: THEREIN.

; NUMBER OF SEQUENCES: 40

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: CUSHMAN DARBY & CUSHMAN

; STREET: 1615 L STREET, N.W.

; CITY: WASHINGTON

; STATE: D.C.

; COUNTRY: U.S.A.

; ZIP: 20036-5601

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: PCT/US92/00282

; FILING DATE: 19920110

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: SCOTT, WATSON T.

; REGISTRATION NUMBER: 26581

; REFERENCE/DOCKET NUMBER: 91532-PCT

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 202-861-3000

; TELEFAX: 202-822-0944

; TELEX: 6714627 CUSH

; INFORMATION FOR SEQ ID NO: 7:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 529 amino acids

; TYPE: AMINO ACID

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: protein

PCT-US92-00282-7

Query Match 21.7%; Score 600; DB 5; Length 529;

Best Local Similarity 28.3%; Pred. No. 4.8e-55;

Matches 155; Conservative 105; Mismatches 222; Indels 66; Gaps 14;

Qy 8 LLVGFL--LPGVLLSEAAKILTISTVGGSHYLLMDRVSQILQDHGHNVTMLNHNKRGPFM 64



; TYPE: PRT  
; ORGANISM: Human  
US-09-813-918-2

Query Match 18.8%; Score 521; DB 4; Length 454;  
Best Local Similarity 28.7%; Pred. No. 1e-46;  
Matches 128; Conservative 79; Mismatches 173; Indels 66; Gaps 13;

```
Qy      118 ALQCSHFLNRKDIMDSLKNENFDMVIVET-----FDYCPFLIAEKLGKPPFVAILSTSFGS 172
          | : ||::| | |: |      :: :: :      ||      :
Db      30 AAAYSHWMNMKTILKELVQRGHEVTVLASSASILFD-----PNDAST 71

Qy      173 LEFGLPIPLSYVPV-FRSLTDMHDFWGRVK--NFLMFFS-----FCR-- 212
          |:| : | | | ::: : | : : |:| :||      ||:
Db      72 LKFEV-YPTSLTKTEFENIIMQQVKRWSDIRKDSFWLYFSQEQEILWELYDIFRNECKDV 130

Qy      213 -----RQQHMQSTFDNTIKEH-FTEGS-----RP-VLSHLLLKAELWFINSDFAFD 256
          :: : || : | | |      || | : ||::| : : ::|
Db      131 VSNKKVMKKLQELRFDIVFADAVFPCGELLAALLNIRPTTLFETMGKADIWLMRNPWSFQ 190

Qy      257 FARPLLNTVYVGGLMEKPIKVPQDLENFIAKFGDSGFVLVTLGSMVNTCQNPEIFKEM 316
          | | ||| :||| || ||:|:::| |: |::| |: :|||::: | :
Db      191 FPHPFLPNVDFVGGFHCKPAKPLPKEMEETFVQSSGENGVVVFSLGSVISN-MTAERANVI 249

Qy      317 NNAFAHLPGQVIWKCQCSEHWPKDVHLAANVKIVDWLPQSDLLAHPsirLFVTHGGQNSIM 376
          | | :|| |:|: : | | | : : |:|:| || | | |:| || | |
Db      250 ATALARIPQKVLWRFDGN---KPDALGLNTRLYKWIPQNDLLGHGPKTRAFITHGGANGIY 306

Qy      377 EAIQHGVPMVGIPFLFGDQPENMVRVEAKKFGVSIQLKKLKAETLALKMKQIMEDKRYKSA 436
          ||| ||:||||||| |||:|: ::|| | : : | :| : : | ||
Db      307 EAIYHGIPMVGIPFLFDQPDNIAHMKAKGAAVRLDENTMSSTDLLNALKTVINDPLYKEN 366

Qy      437 AVAASVILRSHPLSPTQRLVGWIDHVLQTGGATHLKPYVFQQPWHEQYLFDFVFVLLGLT 496
          : | | | : | | | ||: | : || ||: | : : || |||
Db      367 IMKLSRIQHDQPVKPLDRAVFWIEFVMPHKGAKHLRVAADLTWFOYHSLDVGIFLLACV 426

Qy      497 LGTLWLCGKLLGMAVWWLRGARKVKE 522
          ::: | | : ||| |:
Db      427 ATVIFIITKFCLECFW--KFARKGKK 450
```

RESULT 11

US-09-813-918-3

; Sequence 3, Application US/09813918

; Patent No. 6383789

; GENERAL INFORMATION:

; APPLICANT: WEBSTER, Marion et al.

; TITLE OF INVENTION: ISOLATED HUMAN DRUG-METABOLIZING

; TITLE OF INVENTION: PROTEINS, NUCLEIC ACID MOLECULES ENCODING HUMAN

; TITLE OF INVENTION: DRUG-METABOLIZING PROTEINS,

; TITLE OF INVENTION: AND USES THEREOF

; FILE REFERENCE: CL001175

; CURRENT APPLICATION NUMBER: US/09/813,918

; CURRENT FILING DATE: 2001-03-22

; NUMBER OF SEQ ID NOS: 4

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 3

; LENGTH: 288  
; TYPE: PRT  
; ORGANISM: Human  
US-09-813-918-3

Query Match 18.2%; Score 503.5; DB 4; Length 288;  
Best Local Similarity 35.9%; Pred. No. 3.7e-45;  
Matches 104; Conservative 53; Mismatches 126; Indels 7; Gaps 4;

Qy 234 RP-VLSHLLKAEWFINSDFAFDFARPLLNTVYVGGIMEKPIKPVPQDLENFIAKFGD 292  
|| | : ||::| : : ::| | | ||| :||| || ||:|:::| |: |: |:  
Db 1 RPTTLFETMGKADIWLMRNSWSFQFPHFPLPNVDFVGGFHCCKPAKPLPKEMEETFVQSSGE 60  
  
Qy 293 SGFVLVTLGSMVNTCQNPEIFKEMNNAFAHLPGQGVWKCQCSEHWPKDVHLAANKIVDWL 352  
:| |: :||::: | : | | :|| |:| : | | | :| :  
Db 61 NGVVVFSLSGVISN-MTAERANVIATALAKIPQKVLWRFDGN---KPDALGLNTRLYKWI 116  
  
Qy 353 PQSDLLAHPsirLfvthGGQNSIMEAIQHGVPMVGIPLFGDQPENMVRVEAKKFGVSIQL 412  
||:||| || | |:|||| | | ||| ||:||||||| |||:|: :||| | :  
Db 117 PQNDLLGHPKTRAFITHGGANGIYEAIYHGIPMVGIPLFFDQPDNIAHMKAKGAARLDF 176  
  
Qy 413 KKLKAETLALKMKQIMEDKRYKSAAVAASVILRSHPLSPTQRLVGWIDHVLQTGGATHLK 472  
: : | :| :: | || : | | | : | | | ||: |: || ||:  
Db 177 NTMSSTDLLNALKTVINDPLYKENIMKLSRIQHDQPVKPLDRAVFWIEFVMPHKGAKHLR 236  
  
Qy 473 PYVFQQPWHEQYLFDFVFLGLTLGLTLWLCLGKLLGMAVWWLARGARKVKE 522  
| : : || ||| ::: | | : ||| | :  
Db 237 VAAHDLTWFYHSLDVIGFLLACVATVIFIITKFCLFCFW--KFARKGKK 284

RESULT 12

US-09-305-856B-18

; Sequence 18, Application US/09305856B  
; Patent No. 6479236  
; GENERAL INFORMATION:  
; APPLICANT: Penny, Laura  
; APPLICANT: Galvin, Margaret  
; TITLE OF INVENTION: Genotyping the Human  
; TITLE OF INVENTION: UDP-Glucuronosyltransferase 1 (UGT1). Gene  
; FILE REFERENCE: 4389-7 (formerly SEQ-17CIP)  
; CURRENT APPLICATION NUMBER: US/09/305,856B  
; CURRENT FILING DATE: 1999-05-05  
; PRIOR APPLICATION NUMBER: 60/084,807  
; PRIOR FILING DATE: 1998-05-07  
; NUMBER OF SEQ ID NOS: 124  
; SOFTWARE: FastSEQ for Windows Version 3.0  
; SEQ ID NO 18  
; LENGTH: 245  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-305-856B-18

Query Match 13.7%; Score 380; DB 4; Length 245;  
Best Local Similarity 34.8%; Pred. No. 4.5e-32;  
Matches 78; Conservative 49; Mismatches 93; Indels 4; Gaps 2;

Qy 282 DLENFIAKFGDSGFVLVTLGSMVNTCQNPEIFKEMNNAFAHLPGQGVWKCQCSEHWPKDVH 341

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      : | : | | : | | : : | | | : : : : | : | : | : : :
Db      1 EFEAYINASGEHGIVVFSLGSVMSEIPEKKAM-AIADALGKIPQTVLWRYTGT---RPSN 56

Qy      342 LAANVKIVDWLPQSDLLAHPSIRLFVTHGGQNSIMEAIQHGVPMVGIPFLFGDQPENMVRV 401
      | | | : | | | | : | | | | | : | : | : | : | : | : | : | :
Db      57 LANNTILVKWLPQNDLLGHPMTRAFITHAGSHGVYESICNGVPMVMPLFGDQMDNAKRM 116

Qy      402 EAKKFGVSIQLKKLKAETLALKMKQIMEDKRYKSAAVAASVILRSHPLSPTQRLVGWIDH 461
      | | | | : : : : : | | : | : | | : | : : | : | | : :
Db      117 ETKGAGVTLNPLEMTSEDLENALKAVINDKSYKENIMRLSSLHKDRPEPLDLAVFWVEF 176

Qy      462 VLQTTGATHLKPYVFPQWHEQYLFDFVFLGLTLGLTLWLTCGK 505
      | : | | | : | | : : | | | : | : | : | : |
Db      177 VMRHKGAPHLRPAHDLTWYQYHSLDVIGFLLAVVLTVAFITFK 220

```

# RESULT 13

US-08-942-012B-32

```

; Sequence 32, Application US/08942012B
; Patent No. 6235278
; GENERAL INFORMATION:
; APPLICANT: Miller, Lois K.
; APPLICANT: Lu, Albert
; APPLICANT: Dierks, Peter
; APPLICANT: Black, Bruce
; TITLE OF INVENTION: Biological Insect Control Agents Expressing
; TITLE OF INVENTION: Insect-Specific Toxin Genes, Methods and Compositions
; FILE REFERENCE: 28-96a
; CURRENT APPLICATION NUMBER: US/08/942,012B
; CURRENT FILING DATE: 1997-10-01
; PRIOR APPLICATION NUMBER: 08/729,606
; PRIOR FILING DATE: 2000-10-01
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 32
; LENGTH: 515
; TYPE: PRT
; ORGANISM: Spodoptera littoralis nuclear polyhedrosis virus
US-08-942-012B-32

```

```

Query Match          12.5%; Score 346.5; DB 3; Length 515;
Best Local Similarity 22.5%; Pred. No. 5.9e-28;
Matches 122; Conservative 102; Mismatches 211; Indels 107; Gaps 18;

```

```

Qy      20 SEAAKILTI-STVGGSHYLLMDRVSQILQDHGHNVMTL-----NHKRGPFMPDFKKEEKS 73
      | | : : | : | | : | | | : : | | |
Db      16 SAAVRVLCMFPTPSYSHQTVFDVYVNALLRRGHSLVVISPKIHNNHNG----- 63

Qy      74 YQVISWLAPEDHQREFKKSFD-----FF---LEETLGGRGK-----FENLLNV 113
      | : | | | | | | : : | : | : | : | : | : | : | : | :
Db      64 -----HRHHRHENLTEIDVGSVTNNFFKRLQLQDSKVSRRKGIVSDSSTVTRVNYLGL 115

Qy      114 LEYLALQCSHFLNRKDIMDSLK-NENFDMVIVETFDCPFLIAEKLKPFVAILSTSFGS 172
      : : | | : : | : | : | : | : | : | : | : | : | : | :
Db      116 ARMISAQFEH---EQVKRLLRSNQTFDVIVIEAFVSYPLILSYFFKDTPIQISSGHGT 171

Qy      173 LEFGLPIPLSYVPVFRSLLTDHMDFWGRVKNFLMFFSFCRRQQHMQSTFDNTIKEHFTE- 231

```



Db	172	AE-----NFETMGAVARHPVYYPNMWRDRFKGLSVWQTVRQVFTEI	212
Qy	232	-----GSR-PVLSHLLKAEIWFINSDFAFDFARPLLNTVYVG	269
Db	213	RLYMEFSQLDADQSAMMKRQFGSKVPDVALRKNVHMMFVNTHPVFDTNRPVPSNVQYLG	272
Qy	270	GL-MEKPIKPVPQDLENFIAKFGDS---GFVLVTLGSMVNTCQNPEIFKEMNNAFAH---	322
Db	273	GIHIDPAVTSVADEIDNDLAEFLENSTMGVVYVSLGSSVRA---SDMDSNMLNVFVETFR	329
Qy	323	-LPQGVIIWKQCQSHWPKDVHLAANKIVDWLPQSDLLAHPsirLFVTHGGQNSIMEAIQH	381
Db	330	SIPYRVLWKVDKSDKIFD-NIPSNVLIQRWFPQRRVLKHRNVKVFITQGGVQSTDEAIDA	388
Qy	382	GVPMVGIPLFGDQPENMVRVEAKKFGVSIQLKKLKAETLALKMKQIMEDKRYKSAAVAAS	441
Db	389	GVPMFGVPIMGDQFYNVMYETYGIGRGVDTLTVDARQLTEIVMDVADNEKYKNGTLWLR	448
Qy	442	VILRSHPLSPTQRLVGWIDHVLQTGGA-THLKPYPVFQOPWHEQYLFDFVFLGLTLGLTL	500
Db	449	DAIMDQPMRPLEKAVWYTEHVARRKGAKKHLGTRAANVTYISKYAMFDLILPML-ITIFST	507
Qy	501	WL 502	
Db	508	YL 509	

# RESULT 14

US-08-942-012B-33

; Sequence 33, Application US/08942012B

; Patent No. 6235278

## ; GENERAL INFORMATION:

; APPLICANT: Miller, Lois K.

; APPLICANT: Lu, Albert

; APPLICANT: Dierks, Peter

; APPLICANT: Black, Bruce

; TITLE OF INVENTION: Biological Insect Control Agents Expressing

; TITLE OF INVENTION: Insect-Specific Toxin Genes, Methods and Compositions

; FILE REFERENCE: 28-96a

; CURRENT APPLICATION NUMBER: US/08/942,012B

; CURRENT FILING DATE: 1997-10-01

; PRIOR APPLICATION NUMBER: 08/729,606

; PRIOR FILING DATE: 2000-10-01

; NUMBER OF SEQ ID NOS: 33

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 33

; LENGTH: 460

; TYPE: PRT

; ORGANISM: Lacanobia oleracea granulovirus

US-08-942-012B-33

Query Match 12.4%; Score 342.5; DB 3; Length 460;

Best Local Similarity 24.7%; Pred. No. 1.3e-27;

Matches 120; Conservative 93; Mismatches 215; Indels 57; Gaps 18;

Qy	7	LLLVGFLLPGLVLLSEAAILTI-STVGGSHYLLMDRVSQILQDHGHNVTMLNHKRGPFMP	65
----	---	--	----

```

      :||:  :  :|  | || :  |  || :  |  ||||:  |
Db      5 ILLLALAVERIL---CANILCVFPTPAYSHQSVFSAYIDKLSWAGHNVTVIT-----P 54

Qy      66 DFKKEEKSYQVISWLAPEDHQREFK-----KSFDFLEETLGGRGKFENLLNVLEYLALQ 120
      :  :  :||:| | :  |  |  :||  :  :  |:||:
Db      55 MPRAVDHVHQVSSLSVHYFNNLIKNSTMIKKRGVVADETTVTKENYMGLINLV----- 108

Qy      121 CSHFLNRKDIMDSLKNE--NFDMVIVETFDYCPFLIAEKLGKPFVAILSTSFGSLEFGLP 178
      :| :  ::  |:||  ||::|  |  ::  |  ||  |
Db      109 -AHEIKSPNVTRLRLRNKGKFDLIVCEA--YVSYILV-----FGAIYDAPVIQFSSGYA 159

Qy      179 IPLSYVPVFRSLLTDHM---DFWG---RVKNF--LMFFSFCRRQ-QHMQSTFDNTIKEHF 229
      || ::  |  :  :||  :  |  ||  ||  ::  :  :  :| :| |
Db      160 IPENFETVGGEVARNHIKHPNIWRSDFSKSNFEQLMTENYLKNEWALLEKEQENMLKRDF 219

Qy      230 TEGSRPVLSHLLLKAELWFINSDFAFDFARPLLNTVYVGGL-MEKPIKPVPQDLENFIA 288
      |  :  |  :  :||  ||  |  :  |  |:||:  :||  | :|:
Db      220 --GYHDMCQLKSRVLMFLINPAVFDNNRDVSNNIQYLGGIHLKKPRTVRDSRLLSFME 277

Qy      289 KFGDSGFVLVTLGSMVNTC-QNPEIFKEMNNAFAHLPQGVIWKCQCSHWPKDVHL----A 343
      |  |  :  || ::  :  :  |  |  :|  |:||  |  :||  :
Db      278 K--HHIIVYASFGSGIDVLNMDANLIAEFVRVFNNSIPYAVLWKVDSS-----IHLKHNIS 330

Qy      344 ANVKIVDWLPQSDLLAHPSIRLFVTHGGQNSIMEAIQHGVPMVGIPLEFGDQPENMVRVEA 403
      :||  |  || |:|| || |::|| ||  |  ||:  |||:|||: |||  | :|
Db      331 SNVHTQSWFPQRDVLNHPHIKVFITQGGVQSTDEAVNSGVPMIGIPIMGDQFYNVRRYTE 390

Qy      404 KKFGVSIQLKKLKAETLALKMKQIMEDKRYKSAAVAASVILRSHPLSPTQRLVGWIDHVL 463
      |  :  :||:| | |:|| :: :| | :  :  :  | :| :| :| : : :||
Db      391 LGIGEKVNILRLEEGLDRKIKNLVHNKSYELNIKRLNLFISDTPVKPLRKALWFTNYVL 450

Qy      464 QTGGA 468
      :  |
Db      451 RNKDA 455

```

RESULT 15

US-08-942-012B-24

; Sequence 24, Application US/08942012B

; Patent No. 6235278

; GENERAL INFORMATION:

; APPLICANT: Miller, Lois K.

; APPLICANT: Lu, Albert

; APPLICANT: Dierks, Peter

; APPLICANT: Black, Bruce

; TITLE OF INVENTION: Biological Insect Control Agents Expressing

; TITLE OF INVENTION: Insect-Specific Toxin Genes, Methods and Compositions

; FILE REFERENCE: 28-96a

; CURRENT APPLICATION NUMBER: US/08/942,012B

; CURRENT FILING DATE: 1997-10-01

; PRIOR APPLICATION NUMBER: 08/729,606

; PRIOR FILING DATE: 2000-10-01

; NUMBER OF SEQ ID NOS: 33

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 24

; LENGTH: 515

; TYPE: PRT

; ORGANISM: Helicoverpa zea nuclear polyhedrosis virus  
US-08-942-012B-24

Query Match 11.6%; Score 321; DB 3; Length 515;  
Best Local Similarity 24.4%; Pred. No. 3.2e-25;  
Matches 129; Conservative 88; Mismatches 246; Indels 66; Gaps 21;

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Qy      6 VLLLVGFLLPGVLLSEAAKILTISTVGG-SHYLLMDRVSQILQDHGHNVTMLNHKRGPFM 64
      :| | | | | | | | : | : | | : | | : : : : | | : : | |
Db      8 MLLLVLFL--SVL--DGARILCVFPVPSYSHHAVFEAYTNALASRGHTIVRIT----PF- 58

Qy     65 PDFKKEEKSYQVISWLAPEDH-----QREFKKSFDFFLEETLGGRGKFENLLNVLEYL 117
      | | : : : : : | : | | | | | | | : : | | : |
Db     59 PTKKNDSSNVTDVDVLSKDYFKSLVDRSRLFKK-----RGVISETSSVTARN 106

Qy    118 ALQCSHFLNRKDIMDSLK-----NENFDMVIVETF-DYCPFLIAEKL GK-PFVAI----- 165
      : | | : : : | | | | : : | | | | : : | | : |
Db    107 YISLVHMLIDQFSVESVRQLIESNNVFDLLVTEAFLDY-PLVFSHLFGDVPVIQISSGHA 165

Qy    166 LSTSFGSLEFGLPIPLSYVPVFRSLTDMDFWGRV----KNFLMFFSFCCRQOQHMOSTF 221
      | : : | : | : : | : : | : : : : | : : | |
Db    166 LAENFETMGAVSRHPITYPNLWRNKF-QNLNVWEIITEIYTELVLYLEFARLADE----- 219

Qy    222 DNTIKEHFTEGSRPVLSHLLLKAEWFINSDFAFDFARPLLENTVYVGGIMEKPIKPV-- 279
      : | : | : | : : | | : : | | : | : | | |
Db    220 QTKMLRHQFGPNTPSVEELRQVRQLLFVNTHPLFDNNRPVPPSVQYLGSLHLDRNNDVDE 279

Qy    280 PQDLENFIAKF---GDSGFVLVTLGSMVNTC-QNPEIFKEMNNAFAHLPGQVIWKQCQSH 335
      | : : : | : | | : : : : | | | | | : : |
Db    280 QQTMDYNLMQFLNNSTNGVVYSFGTSIRVSDMDDEFLFEFITAFAKQLPYNILWK--TDG 337

Qy    336 WPKDVHLAANVKIVDWLPQSDLLAHPSIRLFVTHGGQNSIMEAIQHGVPMVGIPFLFGDQP 395
      | : | | | | | : | : : | | | | | | | | : : | | |
Db    338 MPMEHVL PKNVLTQTWLPQHHLV LKHSNVVAFVTQGGMQSTDEAIDACVPLIGIPFMGDQA 397

Qy    396 ENMVRVEAKKFGVSIQLKKLKAETL--ALKMKQIMEDKRYKSAAVAASVILRSHPLSPTQ 453
      | : | | : : | : | | : : | | | : : | :
Db    398 YNTNKYEELGIGRNLDPVTLTSHILVSAVLDTVNNKSRYT DNIKALNRSTNYRTRK PME 457

Qy    454 RLVGWIDHVLQTGGATHLKPYVFQQPWHEQYLFDDV FV----FLLGLTLG 498
      : : : : | : | | : : | : | | : : | |
Db    458 KAIWYTEHVIDNGKNPILKTKAANVSYSKYMSDIIVPVITFLVMTHLG 506
```

Search completed: May 7, 2004, 17:33:56  
Job time : 23 secs

OM protein - protein search, using sw model

Run on: May 7, 2004, 17:29:09 ; Search time 21 Seconds  
 (without alignments)  
 2395.627 Million cell updates/sec

Title: US-10-017-867A-282  
 Perfect score: 2768  
 Sequence: 1 MAGQRVLLLVGFLLPGVLLS.....GKLLGMAVWVWLRGARKVKET 523

Scoring table: BLOSUM62  
 Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0  
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 45 summaries

Database : PIR\_78:\*  
 1: pirl:\*  
 2: pir2:\*  
 3: pir3:\*  
 4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	% Query		Match Length	DB	ID	Description
	Score	Match				
1	700	25.3	541	2	JC5423	2-hydroxyacylsphin
2	684	24.7	541	2	A48801	2-hydroxyacylsphin
3	679	24.5	533	2	A39092	glucuronosyltransf
4	674.5	24.4	530	2	A40467	glucuronosyltransf
5	671	24.2	529	2	A42233	glucuronosyltransf
6	670	24.2	531	2	B47113	glucuronosyltransf
7	662.5	23.9	530	2	C47113	glucuronosyltransf
8	658	23.8	531	2	A35343	glucuronosyltransf
9	658	23.8	535	2	I57961	glucuronosyltransf
10	656.5	23.7	528	2	JN0619	glucuronosyltransf
11	654.5	23.6	529	2	A35366	glucuronosyltransf
12	650	23.5	527	2	S15089	glucuronosyltransf
13	649	23.4	530	2	A48633	glucuronosyltransf

14	642	23.2	528	2	JN0620	UDP-glucuronosyltr
15	640	23.1	530	2	S07390	glucuronosyltransf
16	639	23.1	530	2	A36276	glucuronosyltransf
17	637.5	23.0	530	2	S00163	glucuronosyltransf
18	632.5	22.9	530	2	S68200	glucuronosyltransf
19	632	22.8	523	2	S11309	glucuronosyltransf
20	629	22.7	531	2	A31340	glucuronosyltransf
21	623	22.5	530	2	JC5656	UDP glucuronosyltr
22	622.5	22.5	529	2	JE0200	orphan UDP-glucuro
23	612.5	22.1	531	2	A55788	glucuronosyltransf
24	610	22.0	530	2	S17512	glucuronosyltransf
25	600	21.7	529	2	A24600	glucuronosyltransf
26	596.5	21.5	531	2	B55788	glucuronosyltransf
27	513	18.5	485	2	T13694	glucuronosyltransf
28	471	17.0	949	2	T18591	hypothetical prote
29	455.5	16.5	534	2	T34455	hypothetical prote
30	449	16.2	531	2	T33980	hypothetical prote
31	448	16.2	573	2	T27578	hypothetical prote
32	447	16.1	531	2	T23835	hypothetical prote
33	441.5	16.0	508	2	T03910	UDP-glucuronosyltr
34	438	15.8	534	2	T19944	hypothetical prote
35	427	15.4	586	2	T19075	hypothetical prote
36	424	15.3	534	2	T19951	hypothetical prote
37	419	15.1	533	2	T34458	hypothetical prote
38	412.5	14.9	475	2	T33979	hypothetical prote
39	412.5	14.9	537	2	T25536	hypothetical prote
40	411	14.8	745	2	T23893	hypothetical prote
41	409.5	14.8	661	2	T32518	hypothetical prote
42	408	14.7	533	2	T34457	hypothetical prote
43	405.5	14.6	520	2	T19661	hypothetical prote
44	405	14.6	530	2	T18596	hypothetical prote
45	398.5	14.4	526	2	T25535	hypothetical prote

#### ALIGNMENTS

##### RESULT 1

JC5423

2-hydroxyacylsphingosine 1-beta-galactosyltransferase (EC 2.4.1.45) - human

N;Alternate names: UDP-galactose:ceramide galactosyltransferase

C;Species: Homo sapiens (man)

C;Date: 10-Jun-1997 #sequence\_revision 18-Jul-1997 #text\_change 26-Aug-1999

C;Accession: JC5423

R;Kapitonov, D.; Yu, R.K.

Biochem. Biophys. Res. Commun. 232, 449-453, 1997

A;Title: Cloning, characterization, and expression of human ceramide galactosyltransferase cDNA.

A;Reference number: JC5423; MUID:97242209; PMID:9125199

A;Accession: JC5423

A;Molecule type: mRNA

A;Residues: 1-541 <KAP>

A;Cross-references: GB:U62899

A;Experimental source: fetal glioma cell

C;Comment: This enzyme catalyzes the final step of galactosylceramide synthesis.

C;Genetics:

A;Gene: cgt

C;Superfamily: glucuronosyltransferase

C;Keywords: glycoprotein; glycosyltransferase; hexosyltransferase

F;472-492/Domain: hydrophobic #status predicted <HYD>

F;538-540/Region: endoplasmic reticulum retention signal #status atypical

F;78,333,442/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 25.3%; Score 700; DB 2; Length 541;  
Best Local Similarity 32.2%; Pred. No. 6.5e-47;  
Matches 166; Conservative 95; Mismatches 185; Indels 70; Gaps 12;

```
Qy      13 LLPGVLLSEAAKILTISTV-GGSHYLLMDRVSQILQDHGHN-VTMLNHKRGPFMPDFKKE 70
      |  | ::|||: : : || : :: | : ||: | :|: |
Db      11 LWSAVGIAKAAKIIIVPPIMFESHMYIFKTLASALHERGHHTVFLLEGRD----- 61

Qy      71 EKSQVISWLAPEDHQ--REFKKSF-----DFFLEETL----GGRGKFENLLNVLEYLAL 119
      :|| :| : : | | ||: : || : | ::|:
Db      62 -----IAPSNHYSLQRYPGIFNSTTSDAFLQSKMRNIFSGRLTAIELFDILDHYTK 112

Qy     120 QCSHFLNRKDIMDSLKNENFDMVIVETFDYCPFLIAEKLKGPFAVAILSTSFGSLEFGLPI 179
      | : :: || | ||::|: | | |:|| || : : : | | |
Db     113 NCDMMVGNHALIQGLKKEKFDLLLVDPNDMCGFVIAHLLGVKYAVFSTGLWYPAEVGAPA 172

Qy     180 PLSYVPVFRSLLTDHMDFWGRVKN-----FLMFFSFCRRQQHM-----QSTFD 222
      ||:| | | | | | | : | : | | | | | | : | : |
Db     173 PLAYVPEFNSLLTDRMNLQRMKNTGVYLISRLGVSFLVLPKYERIMQKYNLLPEKSMYD 232

Qy     223 NTIKEHFTEGSRPVLSHLLLKAELWFINSDFAFDFARPLLNTVYVGGLMEKPIKVPVQD 282
      | : : || : : | | : | | | | | | | : | | : |
Db     233 -----LVHGSSLWMLCTDVALEFFRPTLPNVVYVGGILTKPASPLPED 275

Qy     283 LENFIAKFGDSGFVLVTLGSMVNTCQNPEIFKEMNNAFAHLPQGVWKQCQSHWPKDVHL 342
      | : :: : | | | | : | : : | : | | | | : | | : |
Db     276 LQRWVNGANEHGFVLVSFGAGVKYL-SEDIANKLAGALGRLPQKVIWRFS---GPKPKNL 331

Qy     343 AANVKIVDWLPQSDLLAHPSIRLFVTHGGQNSIMEAIQHGVPVMVGIPLFGDQPENMVRVE 402
      | | ::| | | | | | | | : | | : | | | | | | : | | :
Db     332 GNNTKLI EWLPQNDLLGHGSKIAFVSHGGLNSIFETMYHGVPPVVGIPVFGDHYDTMTRVQ 391

Qy     403 AKKFGVSIQLKKLKAETLALKMKQIMEDKRYKSAAVAASVILRSHPLSPTQRLVGWIDHV 462
      || | : :: | : : | : :: : : | : | | : | | | : | | :
Db     392 AKGMGILLEWKTVTEKELYEALVKVINNPYSYRQRAQKLSEIHKDQPGHPVNRTIYWIDYI 451

Qy     463 LQTGGATHLKPYPVFQQPWHEQYLFQV-FVFLGLGLTL 497
      :: || ||: | | : : : | | : || | | |
Db     452 IRHNGAHLRAAVHQISFCQYFLLDIAFVLLLGAAL 487
```

## RESULT 2

A48801

2-hydroxyacylsphingosine 1-beta-galactosyltransferase (EC 2.4.1.45) precursor - rat

N;Alternate names: UDPgalactose-ceramide galactosyltransferase

C;Species: Rattus norvegicus (Norway rat)

C;Date: 07-Apr-1994 #sequence\_revision 18-Nov-1994 #text\_change 05-Nov-1999

C;Accession: A48801; I56576; S63480

R;Schulte, S.; Stoffel, W.

Proc. Natl. Acad. Sci. U.S.A. 90, 10265-10269, 1993

A;Title: Ceramide UDPgalactosyltransferase from myelinating rat brain: purification, cloning, and expression.  
A;Reference number: A48801; MUID:94052143; PMID:7694285  
A;Accession: A48801  
A;Status: preliminary  
A;Molecule type: mRNA; protein  
A;Residues: 1-541 <SCH>  
A;Cross-references: GB:L21698; NID:g437665; PIDN:AAA16108.1; PID:g437666  
A;Experimental source: brain  
A;Note: sequence extracted from NCBI backbone (NCBIN:139520, NCBIP:139522)  
R;Stahl, N.; Jurevics, H.; Morell, P.; Suzuki, K.; Popko, B.  
J. Neurosci. Res. 38, 234-242, 1994  
A;Title: Isolation, characterization, and expression of cDNA clones that encode rat UDP-galactose:ceramide galactosyltransferase.  
A;Reference number: I56576; MUID:94358923; PMID:7521399  
A;Accession: I56576  
A;Status: preliminary; translated from GB/EMBL/DDBJ  
A;Molecule type: mRNA  
A;Residues: 1-541 <RES>  
A;Cross-references: EMBL:U07683; NID:g464025; PIDN:AAA50212.1; PID:g464026  
R;Schulte, S.; Stoffel, W.  
Eur. J. Biochem. 233, 947-953, 1995  
A;Title: UDP galactose:ceramide galactosyltransferase and glutamate/aspartate transporter: copurification, separation and characterization of the two glycoproteins.  
A;Reference number: S63480; MUID:96085162; PMID:8521863  
A;Accession: S63480  
A;Molecule type: protein  
A;Residues: 21-28,'A',30-31,'Q',33-39;73-77,'X',79-87;155-166,'Q',168-173;315-322;330-331,'EX',334-338,'Q',340-353;416-423;510-515 <SUL>  
A;Experimental source: brain  
C;Function:  
A;Description: transfers galactose from UDP-galactose to ceramide  
C;Superfamily: glucuronosyltransferase  
C;Keywords: glycoprotein; glycosyltransferase; hexosyltransferase  
F;1-20/Domain: signal sequence #status predicted <SIG>  
F;21-541/Product: 2-hydroxyacylsphingosine 1-beta-galactosyltransferase #status experimental <MAT>  
F;78,333/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 24.7%; Score 684; DB 2; Length 541;  
Best Local Similarity 32.2%; Pred. No. 1.2e-45;  
Matches 165; Conservative 94; Mismatches 184; Indels 70; Gaps 12;

Qy	13	LLPGVLLSEAAKILTISTV-GGSHYLLMDRVSQILQDHGHN-VTMLNHKRGPFMPDFKKE	70
		: :     : : : .    : : :   :    :   :   :	
Db	11	LWSAVGIARAANKIIVPPIMFESHLYIFKTLASALHERGHHTVFLLEGRD-----	61
Qy	71	EKSQYVISWLPEDHQ--REFKKSF-----DFFLEETL----GGRGKFENLLNVLEYLAL	119
		:   :   : :        : :    : : :   : :	
Db	62	-----IDPSNHYSLQRYPGIFNSTTSDAFLQSKMRNIFSGRLTAVELVDILDHYTK	112
Qy	120	QCSHFLNRKDIMDSLKNENFDMVIVETFDYCPFLIAEKLKGPVFVAILSTSFGSLFGLPI	179
		: : : :         : :       :     : : :	
Db	113	NCDMMVGNQALIQLKKEKFDLLLVDPNDMCGFVIAHLLGVKYAVFSTGLWYPAEVGAPA	172
Qy	180	PLSYVPVFRSLLTDHMDFWGRVKN-----FLMFFSFCRRQQH-----MQSTFD	222

```

Db      173  PLAYVPEFNSLLTDRMNFLERMKNTGVYLISRMGVSFIVLPKYERIMQKYNLLPAKSMYD 232
Qy      223  NTIKEHFTEGSRPVLSHLLKAEWFINSDFAFDFARPLLNTVYVGGLMKPIKPVPQD 282
      | : : | | : : | | : | | | | | | | : | | | : |
Db      233  -----LVHGSSLWMLCTDVALEFPRPTLPNVVYVGGILTKPASPLPED 275
Qy      283  LENFIAKFGDSGFVLVTLGSMVNTCQNPEIFKEMNNAFAHLPQGVWKCQC SHWPKDVHL 342
      | : : : | | | | : | : : | | | | : : | : |
Db      276  LQRWVDGAQEHGFVLVSFGAGVKYL-SEDIANKLAGALGRLPQKVIWRFSGT---KPKNL 331
Qy      343  AANVKIVDWLPQSDLLAHPsirLfvTHGGQNSIMEAIQHGVPMVGIPLEFGDQPENMVRVE 402
      | | : : | | | | | | | | | | | | | | | | | | : | | |
Db      332  GNNTKLIEWLPQNDLLGHSNIRAFLSHGGLNSIFETMYHGVPPVVGIPLEFGDHYDTMTRVQ 391
Qy      403  AKKFGVSIQLKKLKAETLALKMKQIMEDKRYKSAAVAASVILRSHPLSPTQRLVGWIDHV 462
      | | | : : : | : : : : | : | | | : | | | | | : :
Db      392  AKGMGILLEWNTVTEGELYDALVKVINNP SYRQRAQKLSEIHKDQPGHPVNRRTTYWIDYI 451
Qy      463  LQTGGATHLKPYVFQQPWHEQYLFQDV-FVFLLG 494
      | : | | | : | | : : : | | : | | | |
Db      452  LRHDGAHHLRSVHQISFCQYFLLDIAFVLLLG 484

```

# RESULT 3

A39092

glucuronosyltransferase (EC 2.4.1.17) 1 precursor, bilirubin-specific - human  
N;Alternate names: bilirubin UDP-glucuronosyltransferase

C;Species: Homo sapiens (man)

C;Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 29-Sep-1999

C;Accession: A39092; E42586; A48887

R;Ritter, J.K.; Crawford, J.M.; Owens, I.S.

J. Biol. Chem. 266, 1043-1047, 1991

A;Title: Cloning of two human liver bilirubin UDP-glucuronosyltransferase cDNAs  
with expression in COS-1 cells.

A;Reference number: A39092; MUID:91093210; PMID:1898728

A;Accession: A39092

A;Molecule type: mRNA

A;Residues: 1-533 <RIT>

A;Cross-references: GB:M57899; NID:g184472; PIDN:AAA63195.1; PID:g184473

R;Ritter, J.K.; Chen, F.; Sheen, Y.Y.; Tran, H.M.; Kimura, S.; Yeatman, M.T.;  
Owens, I.S.

J. Biol. Chem. 267, 3257-3261, 1992

A;Title: A novel complex locus UGT1 encodes human bilirubin, phenol, and other  
UDP-glucuronosyltransferase isozymes with identical carboxyl termini.

A;Reference number: A42586; MUID:92147680; PMID:1339448

A;Accession: E42586

A;Status: preliminary; not compared with conceptual translation

A;Molecule type: nucleic acid

A;Residues: 1-288 <RI2>

A;Cross-references: GB:M84125; NID:g340131; PIDN:AAA61248.1; PID:g340132

A;Note: sequence extracted from NCBI backbone (NCBIP:81433)

R;Ritter, J.K.; Yeatman, M.T.; Kaiser, C.; Gridelli, B.; Owens, I.S.

J. Biol. Chem. 268, 23573-23579, 1993

A;Title: A phenylalanine codon deletion at the UGT1 gene complex locus of a  
Crigler-Najjar type I patient generates a pH-sensitive bilirubin UDP-  
glucuronosyltransferase.



A;Reference number: A48887; MUID:94043159; PMID:8226884  
 A;Accession: A48887  
 A;Status: preliminary; not compared with conceptual translation  
 A;Molecule type: DNA  
 A;Residues: 161-170,172-180 <RI3>  
 A;Experimental source: liver, Crigler-Najjar type I patient  
 A;Note: sequence extracted from NCBI backbone (NCBIP:138934)  
 C;Genetics:  
 A;Gene: GDB:UGT1A1; UGT1  
 A;Cross-references: GDB:120007; OMIM:191740  
 A;Map position: 2q37-2q37  
 C;Superfamily: glucuronosyltransferase  
 C;Keywords: glycosyltransferase; hexosyltransferase; transmembrane protein

Query Match 24.5%; Score 679; DB 2; Length 533;  
 Best Local Similarity 33.8%; Pred. No. 2.8e-45;  
 Matches 175; Conservative 93; Mismatches 211; Indels 38; Gaps 13;

Qy	8	LLVGFL--PGVLLSEAAKILTISTVGGSHYLLMDRVSQILQDHGHNVTMLNHKRGPFMP	65
		::      ::            :          : :	
Db	11	LVLGLLLCVLGPVVS HAGKILLI-PVDGSHWLSMLGAIQQLQQRGHEIVVL-----AP	62
Qy	66	D---FKKEEKSYQVISWLAPEDHQRE-FKKSF-----DFFLEETLGGRGKFENLL	111
		: ::   : ::       ::     : : : :	
Db	63	DASLYIRDGAFTYTLKTY--PVPFQREDVKESFVSLGHNVFENDSFLQRVI---KTYKKIK	117
Qy	112	NVLEYLALQCSHFLNRKDIMDSLKNENFDMVIVETFDYCPFLIAEKLGKPFVAILSTSFG	171
		:  ::     : :::     : :	
Db	118	KDSAMLLSGCSHLLHNKELMASLAESSFDVMLTDPFLPCSPIVAQYLSLPTVFFLHALPC	177
Qy	172	SLEF---GLPIPLSYVPVFRSLTDMDFWGRVKNFLMFFSFCRRQQHMQSTFDNTIKEH	228
		:           :   :   :	
Db	178	SLEFEATQCPNPFYSYVRPLSSHSDHMTFLQRVKNMLIAFSQNFLCDVVYSPY-ATLASE	236
Qy	229	FTEGSRPVLSHLLLKAELWFINSDFAFDFARPLLNTVYVGGLMKPKPKVPQDLENFIA	288
		: :      :        :   ::    :    :   :   :	
Db	237	FLQ-REVTVQDLLSSASVWLFRSDFVKDYPRPIMPNMVVFVGGINCLHQNPLSQEFEAYIN	295
Qy	289	KFGDSGFVLVTLGSMVNTCQNPEIFKEMNNAFAHLPQGVIWKQCQSHWPKDVHLAANVKI	348
		:     : :    : : : :   :    : : : : :     :	
Db	296	ASGEHGIVVFSLGSMVSEIPEKKAM-AIADALGKIPQTVLWRYTGT---RPSNLANTIL	351
Qy	349	VDWLPQSDLLAHPSIRLFVTHGGQNSIMEAIQHGVPMVGIPLFGDQPENMVRVEAKKFGV	408
		:        :     : :   :   :    :    :    :	
Db	352	VKWLPQNDLLGHPMTRAFITHAGSHGVYESICNGVPMVMMPLFGDQMDNAKRMETKGAGV	411
Qy	409	SIQLKKLKAETLALKMKQIMEDKRYKSAVAASVILRSHPLSPTQRLVGWIDHVLQTGGA	468
		:: : : :     :   :      :   : :   :     :  :  :	
Db	412	TLNVLEMTSEDLENALKAVINDKSYKENIMRLSSLHKDRPVEPLDLAVFWVEFVMRHKA	471
Qy	469	THLKPYVFQQPWHEQYLFDFVFVFLGLTLGLTLWLCCGK	505
		::   :: :        :   : :	
Db	472	PHLRPAADLTWYQYHSLDVIGFLLAVVLTVAFITFK	508

glucuronosyltransferase (EC 2.4.1.17) precursor - rat  
N;Alternate names: UDP-glucuronosyltransferase isoform 53K  
C;Species: Rattus norvegicus (Norway rat)  
C;Date: 07-Feb-1992 #sequence\_revision 07-Feb-1992 #text\_change 17-Nov-2000  
C;Accession: A40467; A23520; S59627; A26064; I55247  
R;Haque, S.J.; Petersen, D.D.; Nebert, D.W.; Mackenzie, P.I.  
DNA Cell Biol. 10, 515-524, 1991  
A;Title: Isolation, sequence, and developmental expression of rat UGT2B2: the gene encoding a constitutive UDP glucuronosyltransferase that metabolizes etiocholanolone and androsterone.  
A;Reference number: A40467; MUID:91369480; PMID:1909872  
A;Accession: A40467  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-530 <HAQ>  
R;Jackson, M.R.; Burchell, B.  
Nucleic Acids Res. 14, 779-795, 1986  
A;Title: The full length coding sequence of rat liver androsterone UDP-glucuronyltransferase cDNA and comparison with other members of this gene family.  
A;Reference number: A23520; MUID:86120371; PMID:3003696  
A;Accession: A23520  
A;Molecule type: mRNA  
A;Residues: 31-158,'E',160-285,'S',287-350,'I',352-362,'I',364-430,'E',432-530 <JAC>  
A;Cross-references: GB:X03478; NID:g57452; PIDN:CAA27198.1; PID:g57453  
A;Note: the authors translated the codon ATT for residue 321 as Asn  
R;Yamashita, A.; Watanabe, M.; Tonegawa, T.; Sugiura, T.; Waku, K.  
Biochem. J. 312, 301-308, 1995  
A;Title: Acyl-CoA binding and acylation of UDP-glucuronosyltransferase isoforms of rat liver: their effect on enzyme activity.  
A;Reference number: S59626; MUID:96077159; PMID:7492328  
A;Accession: S59627  
A;Molecule type: protein  
A;Residues: 24-44 <YAM>  
R;Mackenzie, P.I.  
J. Biol. Chem. 261, 14112-14117, 1986  
A;Title: Rat liver UDP-glucuronosyltransferase. cDNA sequence and expression of a form glucuronidating 3-hydroxyandrogens.  
A;Reference number: A26064; MUID:87033594; PMID:2429951  
A;Accession: A26064  
A;Molecule type: mRNA  
A;Residues: 1-430,'E',432-530 <MAC>  
A;Cross-references: GB:J02589; NID:g207582; PIDN:AAA42314.1; PID:g207583  
A;Experimental source: hepatic  
C;Superfamily: glucuronosyltransferase  
C;Keywords: glycosyltransferase; hexosyltransferase; transmembrane protein  
F;1-23/Domain: signal sequence #status predicted <SIG>  
F;24-530/Product: glucuronosyltransferase #status experimental <MAT>

Query Match 24.4%; Score 674.5; DB 2; Length 530;  
Best Local Similarity 33.5%; Pred. No. 6.3e-45;  
Matches 170; Conservative 86; Mismatches 219; Indels 33; Gaps 13;

Qy 34 SHYLLMDRVSQILQDHGHNVTMLNHKRGPFMPDFKKEEKSYQVISW-LAPEDHQREFKKS 92  
||::: : | ||||: | : :: | :::: | |  
Db 34 SHWMNIKIILDELVQRGHEVTVLKPSAYFFLDPKKSSDLKFEIFSTSIKDELQNHFIKL 93

Qy	93	FDFFL--TLGGRGFENLLNVLEYLALQ-CSHFLNRKDIMDSLKNENFDMVIVET	146
Db	94	LDVWTYELPRDTCLSYSPILQNLVYEFSYFYLSICKDAVSNKQLMTKLQESKFDVLFADP	153
Qy	147	FDYCPFLIAEKLGPVFAILSTSFGLP---IPLSYVPVFRSLLDHMDFWGRVK	202
Db	154	VASCGDLIAELLHIPFLYSLSFSPGHKLEKSIGKFIPLPSYVPVILSGLAGKMTFIDRVK	213
Qy	203	NF--LMFFSF-CRRQQHMQ-STFDNTIKEHFTEGSRPVLSHLLLKAELWFINSDFAFDFA	258
Db	214	NMICMLYFDFWFERLRHKEWDTFYSEIL-----GRPTTVDETMKSKEIWLIRSYWDLKFP	268
Qy	259	RPLLNTVYVGGLMKPKVPQDLENFIAKFGDSGFVLVTLGSMVNTCQNPFIKEMNN	318
Db	269	HPTLPNVDIYIGGLHCKPAKPLPKDMEEFVQSSGEHGVVVSLSGSMVS-----NMTEEKAN	323
Qy	319	----AFAHLPQGVIWKQCQSHWPKDVHLAANVKIVDWLPQSDLLAHPSIRLFVTHGGONS	374
Db	324	AIAWALAQIPQKVLWKFD---GKTPATLGPNTRVYKWLPQNDLLGHPKTAKFVTHGGANG	380
Qy	375	IMEAIQHGVPMVGIPFGDQPENMVRVEAKKFGVSIQLKKLKAETLALKMKQIMEDKRYK	434
Db	381	LYEAIYHGIPMIGIPFGDQPDNIAHMAKGAASVSLNIRTMSKLDFLSALVEVIDNPFYK	440
Qy	435	SAAVAASVILRSHPLSPTQRLVGWIDHVLQTTGGATHLKPYVFQQPWHEQYLFDFVFLLG	494
Db	441	KNVMLLSTIHHDPQMKPLDRAVFWIEFIMRHKGAKHLRPLGHNLPWYQYHSLDVIGFLLT	500
Qy	495	LTLGTLWLWCGK-LLGMAVWWLRGARKVK	521
Db	501	CFAVIAALTVMKCLLFMYRFFVKKEKMMK	528

A;Accession: A24324  
A;Molecule type: mRNA  
A;Residues: 1-407, 'V', 409-529 <MA2>  
A;Cross-references: GB:M13506; NID:g207580; PIDN:AAA42313.1; PID:g207581  
A;Experimental source: liver  
C;Superfamily: glucuronosyltransferase  
C;Keywords: glycosyltransferase; hexosyltransferase; transmembrane protein

Query Match 24.2%; Score 671; DB 2; Length 529;  
Best Local Similarity 32.2%; Pred. No. 1.2e-44;  
Matches 175; Conservative 90; Mismatches 228; Indels 50; Gaps 15;

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Qy      6 VLLLVGFLLPGVLLSEAAKILTISTVGGSHYLLMDRVSQILQDHGHNVTMLNHKRGPFMP 65
      ::||: : ||      |:| | ||: : : | ||||:| :
Db      11 LIQLICYFRPGA-----CGKVLVWPT-EYSHWINIKIILNELAQRGHEVTVLVSSASILIE 65

Qy      66 DFKKEEKSYQVISW-LAPEDHQREFKKSFDFFLE--ETLG---GRGKFENLLN----VLE 115
      |:  ::: | |: | : | | : |||      | : : | |:|
Db      66 PTKESSINFEIYSVPLSKSDLEYSFAKWIDWTRDFETLSIWTYYSKMQKVFNEYSDVVE 125

Qy      116 YLALQCSHFLNRKDIMDSLKNENFDMVIVETFDYCPFLIAEKLKGPFFVAILSTSFG---- 171
      | | : |:| |: ||::: : | |:|| | | | | |
Db      126 NL---CKALIWNKSLMKKLQGSQFDVILADAVGPCGELLAELLKTPLVYSLRFCPGYRCE 182

Qy      172 SLEFGLPIPLSYVPVFRSLTLDHMDFWGRVKNFL--MFFSFCRRQQHMQSTFDNTIKEHF 229
      |||:| |||| | |:| | | |||| | ::| | | : : : :
Db      183 KFSGGLPLPPSYVPVVLSELSDRMTFVERVKNMLQMLYFDF-----WFQPFKEKSWSQFY 237

Qy      230 TE--GSRPVLSHLLLKAELWFINSDFAFDFARPLLNTVYVGGIMEKPIKVPVQDLENFI 287
      :: | |: :: ||::| | : : | ||| :||| || ||:::| |:
Db      238 SDVLGRPTTLTEMMGKADIWLIRTFWDLEFPHFPLPNFDFVGGHLCKPAKPLPREMEEFV 297

Qy      288 AKFGDSGFVLVTLGSMVNTCQNPEIFKEMNNAFAHLPQGVIWKCQCShwPKDVHLAANVK 347
      |: | |: :||| | | : :| | :|| |:| | | :| :
Db      298 QSSGEHGVVVFSLGSMVKNL-TEKANVVASALAQIPQKVVRFD---GKKPDTLGSNTR 353

Qy      348 IVDWLPQSDLLAHPsirLfvTHGGQNSIMEAIQHGVPMVGIPLFGDQPENMVRVEAKKFG 407
      : |::|:| | | : || || | | || |:::| | | | | | | | | | | | : :||
Db      354 LYKWIPQNDLLGHPKTKAFVAHGGTNGIYEAIYHGIPVGIPLFADQPDNINHMBAKGAA 413

Qy      408 VSIQLKKLKAETLALKMKQIMEDKRYKSAAVAASVILRSHPLSPTQRLVGWIDHVLQTTGG 467
      | : | | : |:| | | | : | | | | | | | | | | | | : :|
Db      414 VRVDFSILSTTGLLTALKIVMNDPSYKENAMRLSRIHHDQPVKPLDRAVFWIEYVMRHKG 473

Qy      468 ATHLKPYVFPQWPHEQYLFDFVFLLGLTLGT-----LWLCGKLLGMAVWWLRGARK 519
      | ||: : | : : || || : | | | | | | | | | | :|
Db      474 AKHLRSTLHDLSWFQYHSLDVIGFLLLCVGVVFIITKFCLECCRKTANM-----GKK 526

Qy      520 VKE 522
      ||
Db      527 KKE 529

```

RESULT 6

B47113

glucuronosyltransferase (EC 2.4.1.17) UGT2B13 precursor - rabbit

C;Species: Oryctolagus cuniculus (domestic rabbit)

C;Date: 03-May-1994 #sequence\_revision 03-May-1994 #text\_change 29-Sep-1999  
 C;Accession: B47113  
 R;Tukey, R.H.; Pendurthi, U.R.; Nguyen, N.T.; Green, M.D.; Tephly, T.R.  
 J. Biol. Chem. 268, 15260-15266, 1993  
 A;Title: Cloning and characterization of rabbit liver UDP-glucuronosyltransferase cDNAs. Developmental and inducible expression of 4-hydroxybiphenyl UGT2B13.  
 A;Reference number: A47113; MUID:93315511; PMID:8325897  
 A;Accession: B47113  
 A;Status: preliminary  
 A;Molecule type: mRNA  
 A;Residues: 1-531 <TUK>  
 A;Cross-references: GB:L01081; NID:g165796; PIDN:AAA18020.1; PID:g165797  
 C;Superfamily: glucuronosyltransferase  
 C;Keywords: glycosyltransferase; hexosyltransferase; transmembrane protein

Query Match 24.2%; Score 670; DB 2; Length 531;  
 Best Local Similarity 32.6%; Pred. No. 1.4e-44;  
 Matches 169; Conservative 90; Mismatches 206; Indels 54; Gaps 14;

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Qy      34 SHYLLMDRVSQILQDHGHNVTML-----NHKRG----PFMPDFKKEEKSYQVISW 79
      ||:: | : | || ||:| |:: | | :|::| : |
Db      35 SHWMNMKTILDALVQQGHEVTVLRSSASIVIGSNNESGIKFETFHTSYRKDEIENFFMDW 94

Qy      80 LAPEDHQREFKKSFDFFLE---ETLGGRGKFENLLNVLEYLAL---QCSHFLNRKDIMDS 133
      :| :: :| || : ::| : | : | :|
Db      95 F-----YKMIYNVSIESYWETFS-----LTKMVILKYSDICEDICKEVILNKKLMTK 141

Qy     134 LKNENFDMVIVETFDYCPFLIAEKLKGP-----FVAILSTSGSLEFGLPIPLSYVPV 186
      |: ||:: : :||| | | || : | || ||||
Db     142 LQESRFDVVLADPVSPGGELLAELLKIPLVYSLRGFVGMYLQKHGG---GLLLPPSYVPV 198

Qy     187 FRSLTDMDFWGRVKNFL--MFFSFCRRQQHMQSTFDNTIKEHFTGSRPV--LSHLLLK 243
      | | | | ||:| | ::| | : : :| | || | :|
Db     199 MMSGGLSQMTFMERVQNLLCVLYDFW-FPKFNEKRWDQFYSEVL---GRPVTFLEIMGK 254

Qy     244 AELWFINSDFAFDFARPLLNTVYVGGLMEKPIKPVPQDLENFIAKFGDSGFVLVTLGSM 303
      |:| | | : :| ||||| :||| || ||:|::|::| : | :| :|||
Db     255 ADMWLIRSYWDLEFPRELLNFDFIGGLHCKPAKPLQEMEDFVQSSGEEGVVFSLGSM 314

Qy     304 VNTCQNPEIFKEMNNAFAHLPGQVIWKCQCSHWPKDVHLAANVKIVDWLPQSDLLAHPST 363
      :: | : :| | || |::: | | :| :: |:|::|| ||
Db     315 ISNL-TEERANVIASALALPQKVLWRFE---GKKPDMLGSNTRLYKWIPQNDLLGHPKT 370

Qy     364 RLFVTHGGQNSIMEAIQHGVPMVGIPPLFGDQPENMVRVEAKKFGVSIQLKKLKAETLALK 423
      : |:||| | : ||| ||:||||:||||| :::| ::|| | : || : : |
Db     371 KAFITHGGANGVFEAIYHGIPMVGPLPLFGDQLDNIVYMKAKGA AVKLNLTMTSSADLLNA 430

Qy     424 MKQIMEDKRYKSAAVAASVILRSHPLSPTQRLVGWIDHVLQTGGATHLKPYPVQQPWHEQ 483
      :| :: | || |: | | |: | | ||::|:: || ||: |::
Db     431 LKTVINDPSYKENAMTSLRIHHDQPMKPLDRAVFWIEYVMRHKGAKHLRVA AHDLTWYQY 490

Qy     484 YLFDVFVFLGLTLGLTLWLCLGKLLGMAVWWLRGARKVKE 522
      : || || | :| | : : || | |
Db     491 HSLDVIGFLLACVAITTYLIVKCCLLVYRYVLGAGKKKK 529

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## C47113

Query Match 23.9%; Score 662.5; DB 2; Length 530;  
Best Local Similarity 34.5%; Pred. No. 5.5e-44;  
Matches 161; Conservative 75; Mismatches 209; Indels 21; Gaps 10;

Qy	50	GHNVTMLNHKRGPFMPDKFKEEKSQVVISWLPADHQRE-FKKSFDFLEETLGGRGKFE	108
Db	51	GHEVIVLRNSASIFIDPSKQANIKFETFPPIAATKDDLEDLFVHYVSTWTNARQNSQWKYF	110
Qy	109	NLLNVL--EY---LALQCSHFLNRKDIMDSLKNENFDMVIVETFDYCPFLIAEKLGPFPV	163
Db	111	SLLQKLFSEYSDSCENACKEVVFNKTLMTKLQESRFDILLSDAIGPCGELLAELLKIPFV	170
Qy	164	AILSTSFG----SLEFGLPIPLSYVPVFRSLTTHDMDFWGRVKNFL--MFFSFCRRQQHM	217
Db	171	YSLRFTPGYTMKEYSGGLSVPPSYVPIILSDLSGKMTFMERVNNMLCMLYFDFW-FQMFN	229
Qy	218	QSTFDNTIKEHFTEGSRPV-LSHLLKLAELWFINSDFAFDFARPLLENTVYVGGLMKPI	276
Db	230	KKRWDQFYSEVL---GRPVTFSSELVGKADMWLIRSYWDLEFPPTPLPNIQFVGGHLCKPA	286
Qy	277	KPVPQDLENFIAKFGDSGFVLVTLGSMVNTCQNPEIFKEMNNAFAHLPGQVIWKQCQSHW	336
Db	287	KPLPKEMEETFVQSSGEEGVVVFSLGSMVSN-MTEERANLIASAFALPQKVIWRFD--G	342
Qy	337	PKDVHLAANVKIVDWLPQSDLLAHPISIRLFVTHGGQNSIMEAIQHGVPMVGIPLFGDQPE	396
Db	343	QKPETLGPNTRIYDWIPQNDLLGHPKTKAFVTHGGANGIYEAIHHGIPMVGLPLFGEQPD	402
Qy	397	NMVRVEAKKFGVSIQLKKLKAETLALKMKQIMEDKRYKSAAVAASVILRSHPLSPTQRLV	456
Db	403	NIAHMTAKGAIRLNNWKTMSSEDLNLNAKLTVINDPKYKENVMTLSSIIHHDQPMKPLDRAV	462
Qy	457	GWIDHVLQTGGATHLKPYPVFPQWPWHEQYLFDFVFLGLGLTLGLWL	502
Db	463	FWIEYVMRHKGAKHLRVAHDLTWFAQYHSLDVVGVFLVSCAAFLIFL	508

RESULT 8

A35343

glucuronosyltransferase (EC 2.4.1.17) - rat

C;Species: Rattus norvegicus (Norway rat)

C;Date: 14-Sep-1990 #sequence\_revision 14-Sep-1990 #text\_change 29-Sep-1999

C;Accession: A35343

R;Sato, H.; Koiwai, O.; Tanabe, K.; Kashiwamata, S.

Biochem. Biophys. Res. Commun. 169, 260-264, 1990

A;Title: Isolation and sequencing of rat liver bilirubin UDP-

glucuronosyltransferase cDNA: possible alternate splicing of a common primary transcript.

A;Reference number: A35343; MUID:90274676; PMID:2112380

A;Accession: A35343

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-531 <SAT>

A;Cross-references: GB:M34007; NID:g207578; PIDN:AAA42312.1; PID:g207579

C;Superfamily: glucuronosyltransferase

C;Keywords: glycosyltransferase; hexosyltransferase; transmembrane protein

Query Match 23.8%; Score 658; DB 2; Length 531;  
Best Local Similarity 30.9%; Pred. No. 1.2e-43;  
Matches 171; Conservative 106; Mismatches 211; Indels 66; Gaps 17;

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Qy      1 MAGQRVLLLVGFLLPGVLLSEAAKILTISTVGGSHYLLMDRVSQILQDHGHNVMTLNHKR 60
      : |   |||:  ||   :|  |:| :  : |||:| |  | : |   ||   :|
Db      7 LRGLSGLLLLLLALP---WAEGGKVL-VFPMEGSHWLSMRDVVRELHARGHQAVVL---- 58

Qy     61 GPFMPDFKKEEKSYQVISWLAP---EDHQREF----KKSFD-----FFLEETLGGRGK 106
      | :   | |  : : : : |   |:|||   || |:   ||   ||:  |
Db     59 APEVTVHMKGEDFFTLQTYAFPTYKKEYQREILGNAKKGFEPPQHVFVKTFE--ETMASIKK 116

Qy    107 FENLLNVLEYLALQCSHFLNRKDIMDSLKNENFDMVIVETFDYCPFLIAEKLKGPFVAIL 166
      | :|   |  |:  |: | : :  | : : ||:|: :  | |:|: |  | | |
Db    117 FFDL-----YANSCAALLHNKTLIQQLNSSSFDVVLTDVPVFPCGALLAKYLQIPAVFFL 170

Qy    167 STSFGSLEF---GLPIPLSYVPVFRSLTLDHMFDFWGRVKNFLMFFS---FCRROQHMQST 220
      :   : :   | | ||:|  : : : ||| |  ||| |  :  |  | :  |
Db    171 RSVPCGIDYEATQCPKPSSYIPNLLTMLS DHMTFLQRVKNMLYPLTLKYIC----HLSIT 226

Qy    221 FDNTIKEHFTEGSR---PVLSHLLLKAELWFINSDFAFDFARPLLNTVYVGGLMKPIK 277
      : :   :   ||| |  | :|  || ||: ||: || | : : ||:  |
Db    227 PYESLASSELLQREMSLVEVLSH---ASVWLFRGDFVFDYPRPIMPNMVFIGGINCVIKK 282

Qy    278 PVPQDLENFIAKFGDSGFVLVTLGSMVNTCQNPEIFKEMNNAFAHLPGQVIWKCQC SHWP 337
      |: |: | : :  |: | |: : ||||:  :  |: |  : || : : |:  :
Db    283 PLSQEFEAYVNASGEHGIVVFSLSGSMVSEIPEKKAM-EIAEALGRIPQTLWRYTGT--- 338

Qy    338 KDVHLAANVKIVDWLPQSDLLAHPSIRLFVTHGGQNSIMEAIQHGVPMVGIPLFGDQPEN 397
      : : || |  : | ||||: ||| ||  |: || | : | | | : |||| | : |||| | : |
Db    339 RPSNLAKNTILVKWLPQNDLLGHKPARAFITHSGSHGIYEGICNGVPMVMPLFGDQMDN 398

Qy    398 MVRVEAKKFGVSIQLKKLKAETLALKMKQIMEDKRYKSAAVAASVILRSHPLSPTQRLVG 457
      |:| :  ||: : : : |: |  :| : : : | |  :  | : :  |: |  |
Db    399 AKRMETRGAGVTNLNVEMTADDLENALKTVINNKS YKENIMRLSSLHKDRPIEPLDLAVF 458

Qy    458 WIDHVLQTTGGATHLKPYVFQQPWHEQYLFDFVFVLLGLTLGLTLWL-----CGKLLGM 509

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      |:::|:: | | |::| |:: : | | | | : | :: | | |
Db      459 WVEYVMRHKGAPHLRPAAHDLTWYQYHSLDVIGFLLAIVLTVVFIVYKSCAYGCRKCFG- 517

Qy      510 AVWWLRGARKVKET 523
      | :|::
Db      518 -----GKGRVKKS 525

```

# RESULT 9

I57961

glucuronosyltransferase (EC 2.4.1.17) precursor - rat

N;Alternate names: glucuronosyltransferase 1 B1; morphine UGT

C;Species: Rattus norvegicus (Norway rat)

C;Date: 12-Aug-1996 #sequence\_revision 12-Aug-1996 #text\_change 29-Sep-1999

C;Accession: I57961; S51197; S68333

R;Coffman, B.L.; Green, M.D.; King, C.D.; Tephly, T.R.

Mol. Pharmacol. 47, 1101-1105, 1995

A;Title: Cloning and stable expression of a cDNA encoding a rat liver UDP-glucuronosyltransferase (UDP-glucuronosyltransferase 1.1) that catalyzes the glucuronidation of opioids and bilirubin.

A;Reference number: I57961; MUID:95327065; PMID:7603447

A;Accession: I57961

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-535 <RES>

A;Cross-references: EMBL:U20551; NID:g695161; PIDN:AAC52219.1; PID:g695162

R;Ishii, Y.; Tsuruda, K.; Tanaka, M.; Oguri, K.

Arch. Biochem. Biophys. 315, 345-351, 1994

A;Title: Purification of a phenobarbital-inducible morphine UDP-glucuronosyltransferase isoform, absent from guinea rat liver.

A;Reference number: S51197; MUID:95077409; PMID:7986077

A;Accession: S51197

A;Molecule type: protein

A;Residues: 30-41 <ISH>

R;Ikushiro, S.; Emi, Y.; Iyanagi, T.

Arch. Biochem. Biophys. 324, 267-272, 1995

A;Title: Identification and analysis of drug-responsive expression of UDP-glucuronosyltransferase family 1 (UGT1) isozyme in rat hepatic microsomes using anti-peptide antibodies.

A;Reference number: S68333; MUID:96132654; PMID:8554318

A;Accession: S68333

A;Molecule type: protein

A;Residues: 30-37 <IKU>

C;Genetics:

A;Gene: UGT1.1

C;Superfamily: glucuronosyltransferase

C;Keywords: glycosyltransferase; hexosyltransferase

Query Match 23.8%; Score 658; DB 2; Length 535;

Best Local Similarity 31.4%; Pred. No. 1.3e-43;

Matches 171; Conservative 97; Mismatches 215; Indels 62; Gaps 14;

```

Qy      13 LLPGVLL-----SEAAKILTISTVGGSHYLLMDRVSQILQDHGHNVTMLNHKRGPFMP 65
      ||| :|| | | |::| | : |||:| | | | | | | | | : |
Db      13 LLPCLLLCVLGPSASHAGKLLVI-PIDGSHWLSMLGVIQQLQKKGHEVVVI----APEAS 67

Qy      66 DFKKEEKSYQVISWLPEDHQREFKKSFDFFLEETLGGRGKFEN---LLNVLE----- 115

```



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      || | : : | :: | : | || | : || ::
Db      68 IHIKEGSFYTMRKYPVPFQENENVTA-----FVEL---GRSVFDQDPFLLRVVKTYNKVKR 120
Qy      116 ---YLALQCSHFLNRKDIMDSLKNENFDMVIVETFDYCPFLIAEKLKGKPFVAILSTSFGS 172
      | || | : : | || : || : : | | : : | | | : |
Db      121 DSSMLLSGCSHLLHNAEFMASLEQSHFDALLTDPFLPCGSIVAQYLSLPAVYFLNALPCS 180
Qy      173 LEF---GLPIPLSYVPVFRSLLTDHMDFWGRVKNFLMFFS---FCRRQQHMQSTFDNTIK 226
      | : | || || | | || | : | || | : : | | : |
Db      181 LDLEATQCPAPLSYVPKSLSSNTDRMNFLQRVKNMIIALTENFLCRVVYSPYGLATEIL 240
Qy      227 EHFTEGSRPVLSHLLLKAELWFINSDFAFDFARPLLNTVYVGGLMEKPIKVPQDLENF 286
      : : || | : | : || | : || : || | : || : | : | :
Db      241 Q-----KEVTVKDLLSPASIWLMRNDVFKDYPRPIMPNMVFIGGINCLQKKALSQEFAY 295
Qy      287 IAKFGDSGFVLVTLGSMVNTCQNPEIFKEMNNAFAHLPQGVIWKQCQSHWPKDVHLAANV 346
      : | : | | : : || | : : | : | : || | : : : : || |
Db      296 VNASGEHGIVVFSLGSMVSEIPEKKAM-EIAEALGRIPQTVLWRYTGT---RPSNLAKNT 351
Qy      347 KIVDWLPQSDLLAHPSIRLFVTHGGQNSIMEAIQHGVPMVGIPFLFGDQPENMVRVEAKKF 406
      : | || | : || | | | : || | : | | | : || | : | | :
Db      352 ILVKWLPQNDLLGHPKARAFITHSGSHGIYEGICNGVPMVMMPLFGDQMDNAKRMETRGA 411
Qy      407 GVSIQLKKLKAETLALKMKQIMEDKRYKSAAVAASVILRSHPLSPTQRLVGWIDHVLQTG 466
      || : : : : | : | : | : : | | : | : : | : | | : : :
Db      412 GVTLVNLEMTADDLENALKTVINNKSYKENIMRLSSLHKDRPIEPLDLAVFWVEYVMRHK 471
Qy      467 GATHLKPYPVFQQPWHEQYLFDFVFLGLTLGLTLWL-----CGKLLGMAVWWLRGAR 518
      || || : | | : : || || : | : : | | | |
Db      472 GAPHLRPAHDLTWYQYHSLDVGFLLAIVLTVVFIVYKSCAYGCRKCFG-----GKG 524
Qy      519 KVKET 523
      : || :
Db      525 RVKKS 529

```

# RESULT 10

JN0619

glucuronosyltransferase (EC 2.4.1.17) 2B-4 precursor - human

N;Alternate names: UDP-glucuronosyltransferase 2B-11

C;Species: Homo sapiens (man)

C;Date: 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change 02-Jun-2000

C;Accession: JN0619; A27878

R;Jin, C.J.; Miners, J.O.; Lillywhite, K.J.; Mackenzie, P.I.

Biochem. Biophys. Res. Commun. 194, 496-503, 1993

A;Title: cDNA cloning and expression of two new members of the human liver UDP-glucuronosyltransferase 2B subfamily.

A;Reference number: JN0619; MUID:93326164; PMID:8333863

A;Accession: JN0619

A;Molecule type: mRNA

A;Residues: 1-528 <JIN>

A;Cross-references: GB:AF081793; NID:g3426331

A;Experimental source: liver

R;Jackson, M.R.; McCarthy, L.R.; Harding, D.; Wilson, S.; Coughtrie, M.W.H.; Burchell, B.

Biochem. J. 242, 581-588, 1987

A;Title: Cloning of a human liver microsomal UDP-glucuronosyltransferase cDNA.



RESULT 11

A35366

glucuronosyltransferase (EC 2.4.1.17) UDPGTh-2 precursor - human

C;Species: Homo sapiens (man)

C;Date: 17-Aug-1990 #sequence\_revision 17-Aug-1990 #text\_change 29-Sep-1999

C;Accession: A35366

R;Ritter, J.K.; Sheen, Y.Y.; Owens, I.S.

J. Biol. Chem. 265, 7900-7906, 1990

A;Title: Cloning and expression of human liver UDP-glucuronosyltransferase in COS-1 cells. 3,4-Catechol estrogens and estriol as primary substrates.

A;Reference number: A35366; MUID:90243659; PMID:2159463

A;Accession: A35366

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-529 <RIT>

A;Cross-references: GB:J05428; NID:g340079; PIDN:AAA36793.1; PID:g340080

C;Genetics:

A;Gene: GDB:UGT2B7; UGT2B9

A;Cross-references: GDB:5892203; OMIM:600218

A;Map position: 4q13-4q13

C;Superfamily: glucuronosyltransferase

C;Keywords: glycosyltransferase; hexosyltransferase; transmembrane protein

Query Match 23.6%; Score 654.5; DB 2; Length 529;  
Best Local Similarity 31.5%; Pred. No. 2.3e-43;  
Matches 163; Conservative 88; Mismatches 212; Indels 55; Gaps 14;

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Qy      34 SHYLLMDRVSQILQDHGHNVTMLNHKRG-PFMPD-----FKKEEKSQY---Q 75
      ||:: : : | ||||| | : | |::: |
Db      34 SHWMNIKTILDELIQRGHEVTVLASSASILFDPNNSSALKIEIYPTSLTKTELENFIMQQ 93

Qy      76 VISWL-APEDHQREFKKSFDFFLEETLGGRGKFENLLNVLEYIALQ-CSHFLNRKDIMDS 133
      : | |:| :| : : : :: : : | :| |
Db      94 IKRWSDLPKD-----TFWLYFSQV-----QEIMSIFGDITRKFCCKDVVSNNKKFMKK 139

Qy     134 LKNENFDMVIVETFDYCPFLIAEKLKGKPFVAILSTS----FGSLEFGLPIPLSYVPVFRS 189
      :: ||:: : | |:|| || || | | | | | |
Db     140 VQESRFDVIFADAIFPCSELLAELENIPFVYSLSFSPGYTFEKHSGGFIFPPSYVPVMS 199

Qy     190 LLTDHMDFWGRVKN--FLMFFSFCRRQQHMQSTFDNTIKEHFTE---GSRPVLSHLLLKA 244
      ||| | | |||| ::::| | | : | | | : ||
Db     200 ELTDQMTFMERVKNMIIYVLYDFD-----WFEIFDMKKWDQFYSEVLGRPTTLSETMGKA 253

Qy     245 ELWFINSDFAFDFARPLLNPNTVYVGGLMEKPIKPVPQDLENFIAKFGDSGFVLVTLGSMV 304
      ::| | : : | | |||| :||| || ||:::|::: |::| | :| ||||
Db     254 DVWLIRNSWNFQFPHPLLPNVDFVGGLHCKPAKPLPKEMEDFVQSSGENGVVVFSLGSMV 313

Qy     305 NTCQNPEIFKEMNNAFAHLPGQVIWKQCQSHWPKDVHLAANVKIVDWLPQSDLLAHPsir 364
      : | : :| | :|| |:| : | | | :| :||:| || |
Db     314 SN-MTEERANVIASALAIQIPQKVLWRFDGN---KPDTLGLNTRLYKWIPQNDLLGHPKTR 369

Qy     365 LFVTHGGQNSIMEAIQHGVPMVGIPPLFGDQPENMVRVEAKKFGVSIQLKKLKAETLALKM 424
      |:|||| | | ||| ||:||||||| ||::: :::: | : : : | :
Db     370 AFITHGGANGIYEAIYHGIPMVGIPLFADQPDNIAHMKARGAAVRVDFNTMSSTDLLNAL 429

```

Qy 425 KQIMEDKRYKSAAVAASVILRSHPLSPTQRLVGWIDHVLQTGGATHLKPYVFQQPWHEQY 484  
 |::: | || : | | | : | | | |:: |:: || ||: | : :  
 Db 430 KRVINDPSYKENVMKLSRIQHDQPVKPLDRAVFWIEFVMRHKGAKHLRVAHADLTWFQYH 489  
 Qy 485 LFDVVFVLLGLTLGLTLWLCLGKLLGMAVWWLRGARKVKE 522  
 || ||| ::: | | : ||| |:  
 Db 490 SLDVIGFLLVCVATVIFIVTKCCLEFCFW--KFARKAKK 525

# RESULT 12

S15089

glucuronosyltransferase (EC 2.4.1.17) - rat

C;Species: Rattus norvegicus (Norway rat)

C;Date: 21-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 20-Jun-2000

C;Accession: S15089

R;Lazard, D.; Zupko, K.; Poria, Y.; Nef, P.; Lazarovits, J.; Horn, S.; Khen, M.; Lancet, D.

Nature 349, 790-793, 1991

A;Title: Odorant signal termination by olfactory UDP glucuronosyl transferase.

A;Reference number: S15089; MUID:91156050; PMID:1900353

A;Accession: S15089

A;Molecule type: mRNA

A;Residues: 1-527 <LAZ>

A;Cross-references: GB:X57565; NID:g57762; PIDN:CAA40797.1; PID:g3980217

C;Superfamily: glucuronosyltransferase

C;Keywords: glycosyltransferase; hexosyltransferase

Query Match 23.5%; Score 650; DB 2; Length 527;

Best Local Similarity 31.2%; Pred. No. 5.2e-43;

Matches 166; Conservative 87; Mismatches 205; Indels 74; Gaps 12;

Qy 7 LLLVGFLLPGVLLSEAAKILTISTVGGSHYLLMDRVSQILQDHGHNVTMLNHKRGPFMP- 65  
 | |:: | | : | : ||:: | : : | ||:: | |:  
 Db 12 LSLLGMSLGGNVL-----IWPMEGSHWLNVKIIDIPELLRKEHNVTVLVASGALFITP 63  
 Qy 66 -----DFKKEE-----KSYQVISWL----APEDHQREFKKSFDFFLEETLGG 103  
 | ||: | : |::|| : | : | : | |  
 Db 64 SVSPSLTFEIIYPVPFPGKEKIESVIKDF-VLTWLENRSPSTIWTIFYKEMAKVIEEFHLVS 122  
 Qy 104 RGKFENLLNVLEYLALQCSHFLNRKDIMDSLKNENFDMVIVETFDYCPFLIAEKLKGPV 163  
 || | | : : | | : |::: : | : | || | |:  
 Db 123 RG-----ICDGVLKNEKLMTKLQRGKFEVLLSDPVFPCGDIVALKLGIPFI 168  
 Qy 164 AILSTSFGLSLEFG-----LPIPLSYVPVFRSLLTDHMDFWGRVKNFLMFFSFCR 212  
 || | : | || | | || | | | |:: | : : |  
 Db 169 Y-----SLRFSPASTVEKHCGKVPFPSPSYVPAILSELTDQMSFADRVRNFISY----R 217  
 Qy 213 RQQHMQSTFDNTIKEHFTE--GSRPVLSHLLLKAEIWFINSDFAFDFARPLLNPNTVYVGG 270  
 | : | | ::: | | : ||:: | : : | : | || | | : ||  
 Db 218 MQDYMFETLWKQWDSYYSKALGRPTTLCETMGKAEIWLRTYWDFFPRPYLPNFEEVGG 277  
 Qy 271 LMEKPIKPVPQDLENFIAKFGDSGFVLVTLGSMVNTCQNPEIFKEMNNAFAHLPQGVIVK 330  
 | || ||:: |:: | | : | | : | || | | : : | : | : |:  
 Db 278 LHCKPAKPLPKEMEETFVQTSGEHGTVVFSLSGSMVKNL-TEEKANLIASALAQIPQKVLWR 336  
 Qy 331 CQCSHWPKDVHLAANVKIVDWLPQSDLLAHPSIRLFVTHGGQNSIMEAIQHGVPVVGIP 390  
 : | : | : : ||:: | | | |:: | | | | |:: | : |:

Db 337 YK---GKIPATLGSNTRLFDWIPQNDLLGHPKTRAFITHGGTNGIYEAIYHGIPMVGVPM 393

Qy 391 FGDQPENMVRVEAKKFGVSIQLKKLKAETLALKMKQIMEDKRYKSAAVAASVILRSHPLS 450  
| |||:|: ::|| | : : : : | : : : : || |: | | |:

Db 394 FADQPDNIAHMKAKGAAVEVMNMTSADLLSAVRVINEPFYKENAMRLSRIHHDQPVK 453

Qy 451 PTQRLVGWIDHVLQTTGGATHLKPYVFQQPWHEQYLFDFVFLGLTLGLTLWL 502  
| | | ||: |: : || ||: | : : || ||| : |

Db 454 PLDRAVFWIEFVMRHKGAKHLRVAHDLSWFQYHSLDVIGFLLACMASAILL 505

# RESULT 13

A48633

glucuronosyltransferase (EC 2.4.1.17) precursor - human

N;Alternate names: dihydrotestosterone/androstanediol UDP-

glucuronosyltransferase isoform 3, udpgth-3; UDP glucuronosyltransferase 2 family, protein B15

C;Species: Homo sapiens (man)

C;Date: 07-Apr-1994 #sequence\_revision 18-Nov-1994 #text\_change 29-Sep-1999

C;Accession: A48633; I38559

R;Chen, F.; Ritter, J.K.; Wang, M.G.; McBride, O.W.; Lubet, R.A.; Owens, I.S. Biochemistry 32, 10648-10657, 1993

A;Title: Characterization of a cloned human dihydrotestosterone/androstanediol UDP-glucuronosyltransferase and its comparison to other steroid isoforms.

A;Reference number: A48633; MUID:94002056; PMID:8399210

A;Accession: A48633

A;Status: preliminary; not compared with conceptual translation

A;Molecule type: nucleic acid

A;Residues: 1-530 <CHE>

A;Experimental source: liver

A;Note: sequence extracted from NCBI backbone (NCBIP:138786)

R;Green, M.D.; Oturu, E.M.; Tephly, T.R.

Drug Metab. Dispos. 22, 799-805, 1994

A;Title: Stable expression of a human liver UDP-glucuronosyltransferase (UGT2B15) with activity toward steroid and xenobiotic substrates.

A;Reference number: I38559; MUID:95136867; PMID:7835232

A;Accession: I38559

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 1-530 <RES>

A;Cross-references: EMBL:U08854; NID:g475758; PIDN:AAC50077.1; PID:g475759

C;Genetics:

A;Gene: GDB:UGT2B15; UGT2B8

A;Cross-references: GDB:5892418; OMIM:600219

A;Map position: 4q13-4q13

C;Superfamily: glucuronosyltransferase

C;Keywords: glycosyltransferase; hexosyltransferase

Query Match 23.4%; Score 649; DB 2; Length 530;

Best Local Similarity 31.8%; Pred. No. 6.3e-43;

Matches 155; Conservative 90; Mismatches 218; Indels 24; Gaps 10;

Qy 34 SHYLLMDRVSQILQDHGHNVTMLNHKRGPFMPDFKKEEKSQVI-SWLAPEDHQREFKKS 92

||:| : : | || ||:| : | : | | : |

Db 34 SHWINMKTILEELVQRGHEVTVLTSASTLVNASKSSAIKLEVYPTSLTKNDLEDSLLKI 93

Qy 93 FDFFLEETLGGRGKFENLLNVLEYLALQ-----CSHFLNRKDIMDSLKNENFDMVIV 144

```

      | ::      : | : : | : | :      | : | : | | : | ::::
Db      94 LDRWIYGV--SKNTFWSYFSQLQELCWEYYDYSNKLCKDAVLNKKLMMKLQESKFDVILA 151

Qy      145 ETFDYCPFLIAEKLGPFPVAILSTSEFG-SLE---FGLPIPLSYVPVFRSLLTDHMDFWGR 200
      : : | | : | | | : | | | | | | | : | | | |
Db      152 DALNPCGELLAELFNIPFLYSLRFSVGYTFEKNNGGGLFPSPSYVPVVMSELSQDMIFMER 211

Qy      201 VKNF--LMFFSFCRRQQHMQSTFDNTIKEHFTEGSRPVLSHLLLKAELWFINSDFAFDFA 258
      : | | : : | | : : : | | | | : | | : | : | : |
Db      212 IKNMIHMLYFDFWFQIYDLKK-WDQFYSE--VLGRPTTLFETMGKAEMWLIRTYWDFEFP 268

Qy      259 RPLLNTVYVGGLMEKPIKVPQDLENFIAKFGDSGFVLVTLGSMVNTCQNPEIFKEMNN 318
      | | | | : | | | | | | : : : | : | : | : | : : : | : :
Db      269 RPFLPNVDFVGGGLHCKPAKPLPKEMEETFVQSSGENGIVVFSLGSMISN-MSEESANMIAS 327

Qy      319 AFAHLPQGVIWKCQCSEHWPDKDVHLAANVKIVDWLPQSDLLAHPSIRLFTVTHGGQNSIMEA 378
      | | : | | : | : | | : | : : | | | : | | | | : | : | | |
Db      328 ALAQIPQKVLWRFD---GKKPNTLGSNTRLYKWLQPNDLLGHPKTKAFITHGGTNGIYEA 384

Qy      379 IQHGVPMVGIPFLFGDQPENMVRVEAKKFGVSIQLKKLKAETLALKMKQIMEDKRYKSAAV 438
      | | : | | | | | | | | : : : : | : : : : : | : | : | | :
Db      385 IYHGIPMVGIPFLFADQHDNIAHMKAKGAALSVDIRTMSSRDLLNALKSVINDPVYKENVM 444

Qy      439 AASVILRSHPLSPTQRLVGWIDHVLQTTGGATHLKPYVFQQPWHEQYLFDFVFLGLTLG 498
      | | : | | | | | : : | | | : : | : : | | | |
Db      445 KLSRIHHDQPMKPLDRAVFWIEFVMRHKGAKHLRVAAHNLTWIIQYHSLDVIAFLACVAT 504

Qy      499 TLWLCGK 505
      : : : |
Db      505 VIFIITK 511

```

# RESULT 14

JN0620

UDP-glucuronosyltransferase (EC 2.4.1.-) 2B-10 precursor - human

C;Species: Homo sapiens (man)

C;Date: 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change 28-May-1999

C;Accession: JN0620

R;Jin, C.J.; Miners, J.O.; Lillywhite, K.J.; Mackenzie, P.I.

Biochem. Biophys. Res. Commun. 194, 496-503, 1993

A;Title: cDNA cloning and expression of two new members of the human liver UDP-glucuronosyltransferase 2B subfamily.

A;Reference number: JN0619; MUID:93326164; PMID:8333863

A;Accession: JN0620

A;Molecule type: mRNA

A;Residues: 1-528 <JIN>

A;Cross-references: GB:X63359; NID:g516149; PIDN:CAA44961.1; PID:g516150

A;Experimental source: liver

C;Superfamily: glucuronosyltransferase

C;Keywords: glycoprotein; glycosyltransferase; hexosyltransferase; transmembrane protein

F;1-23/Domain: signal sequence #status predicted <SIG>

F;24-528/Product: UDP-glucuronosyltransferase 2B-10 #status predicted <MET>

F;491-508/Domain: transmembrane #status predicted <TMM>

F;66,314,481/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match

23.2%; Score 642; DB 2; Length 528;

Best Local Similarity 31.6%; Pred. No. 2.2e-42;  
Matches 167; Conservative 82; Mismatches 213; Indels 66; Gaps 13;

```
Qy      31 VGGSHYLLMDRVSQILQD---HGHNVTMLNHKRGPFMPDFKKEEKSYQVISWLAPEDHQR 87
      | : | | : |:: | | |:: | : : | |
Db      27 VWAAEYSLWMNMKTILKELVQRGHEVTVL-----ASSASIL--FDPNDSST 70

Qy      88 EFKKSFDFFLEETLGGRGKFENLLNVL-----EYLALQ 120
      : : | : | : |:: | : :
Db      71 LKLEVYPTSLTKT-----EFENIIMQLVKRLSEIQKDTFWLPFSQEQEILWAINDIIRNF 125

Qy     121 CSHFLNRKDIMDSLKNENFDMVIVETFDYCPFLIAEKLKGKPFVAILSTSGF--SLE---FG 176
      | : : | : | | : |:: | : : | |:: | | | | | | |
Db     126 CKDVVSNKKLMKKLQESRFDIVFADAYLPCGELLAELFNIPFVYSHSFSPGYSFERHSGG 185

Qy     177 LPIPLSYVPVFRSLLTDHMDFWGRVKN--FLMFFSFCCRQOQHMOSTFDNTIKEHFTEGSR 234
      | | | | | | | : | | | | | | : : : | | : : | : | |
Db     186 FIFPPSYVPVVMKSLSDQMTFMERVKNMPLYVLYDFDFWQIFNMKK-WDQFYSE--VLGRP 242

Qy     235 PVLSHLLLKAEWFINSDFAFDFARPLLPTVYVGGLEKPIKPVFQDLENFIAKFGDSG 294
      | | : |:: | : : : | | | | | : | | | | | | : | : |
Db     243 TTLSETMRKADIWLMRNSWNFKFPHFPLPNVDFVGGHLHCKPAKPLPKEMEEFVQSSGENG 302

Qy     295 FVLVTLGSMVNTCQNPEIFKEMNNAFAHLPQGVIWKCQCQSHWPKDVHLAANKIVDWLPQ 354
      | : : | | | : | : | : | | : | : | : | : | : |
Db     303 VVVFSLGSMVSN-MTEERANVIATALAKIPQKVLWRFDGN---KPDALGLNTRLYKWIPQ 358

Qy     355 SDLLAHPsirLFVTHGGQNSIMEAIQHGVPMVGIPLFQDQPENMVRVEAKKFGVSIQLKK 414
      : | | | | | | | : | | | | | | | | | : | : | : | : |
Db     359 NDLLGHPKTRAFITHGGANGIYEAIYHGIPMVGIPLFQDQPDNIAHMKAKGAAVRVDFNT 418

Qy     415 LKAETLALKMKQIMEDKRYKSAAVAASVILRSHPLSPTQRLVGWIDHVLQTTGATHLPKY 474
      : : | : : | | : | | : | | | | : | : | : | : |
Db     419 MSSTDLLNALKTVINDPYKENIMKLSRIQHDQPVKPLDRAVFWIEFVMRHKGAKHLRVA 478

Qy     475 VFQQPWHEQYLFDFVFLGLTLGLTLWLCGKLLGMAVWWLRGARKVKE 522
      | : : | | | | : : | : | : | | : |
Db     479 AHNLTWFQYHSLDVIGFLLACVATVLFIIITKCCLFCFW--KFARKGKK 524
```

#### RESULT 15

S07390

glucuronosyltransferase (EC 2.4.1.17) 3 precursor - rat

N;Alternate names: 17beta-hydroxysteroid UDP-glucuronosyltransferase; UDP-glucuronosyltransferase isoform 50K

C;Species: Rattus norvegicus (Norway rat)

C;Date: 30-Sep-1991 #sequence\_revision 30-Sep-1991 #text\_change 07-May-1999

C;Accession: S07390; A33236; A28460; S59626

R;Harding, D.; Wilson, S.M.; Jackson, M.R.; Burchell, B.; Green, M.D.; Tephly, T.R.

Nucleic Acids Res. 15, 3936, 1987

A;Title: Nucleotide and deduced amino acid sequence of rat liver 17beta--hydroxysteroid UDP-glucuronosyltransferase.

A;Reference number: S07390; MUID:87231096; PMID:3108864

A;Accession: S07390

A;Molecule type: mRNA

A;Residues: 1-530 <HAR>

A;Cross-references: EMBL:Y00156  
 A;Experimental source: liver  
 A;Accession: A33236  
 A;Molecule type: protein  
 A;Residues: 24-61 <HAR2>  
 A;Experimental source: liver  
 R;Mackenzie, P.I.  
 J. Biol. Chem. 262, 9744-9749, 1987  
 A;Title: Rat liver UDP-glucuronosyltransferase. Identification of cDNAs encoding two enzymes which glucuronidate testosterone, dihydrotestosterone, and beta-estradiol.  
 A;Reference number: A28460; MUID:87250645; PMID:3110162  
 A;Accession: A28460  
 A;Molecule type: mRNA  
 A;Residues: 1-118,'G',120-240,'L',242-423,'S',425-499,'T',501-530 <MAC>  
 A;Experimental source: liver  
 R;Yamashita, A.; Watanabe, M.; Tonegawa, T.; Sugiura, T.; Waku, K.  
 Biochem. J. 312, 301-308, 1995  
 A;Title: Acyl-CoA binding and acylation of UDP-glucuronosyltransferase isoforms of rat liver: their effect on enzyme activity.  
 A;Reference number: S59626; MUID:96077159; PMID:7492328  
 A;Accession: S59626  
 A;Molecule type: protein  
 A;Residues: 24-44 <YAM>  
 A;Experimental source: liver  
 C;Superfamily: glucuronosyltransferase  
 C;Keywords: glycosyltransferase; hexosyltransferase; transmembrane protein  
 F;1-23/Domain: signal sequence #status predicted <SIG>  
 F;24-530/Product: glucuronosyltransferase #status experimental <MAT>  
 F;494-510/Domain: transmembrane #status predicted <TMM>

Query Match 23.1%; Score 640; DB 2; Length 530;  
 Best Local Similarity 34.2%; Pred. No. 3.2e-42;  
 Matches 167; Conservative 81; Mismatches 189; Indels 52; Gaps 15;

Qy	34	SHYLLMDRVSQILQDHGHNVT-----MLNHKRGPFMPDFKKEEKSYQVISWLPAPEDH	85
		: : :         :   :         : : :	
Db	34	SHWMNIKTILDELVQRGHEVTVLKPSAYYVLDPKKS---PDLKFETFPSTV----SKDEL	86
Qy	86	QREFKKSFDFFLEE-----TLGGRGKFENLLNVLE--YLALQCSHFLENRKDIMDSLKNEN	138
		:       :     :   : :     :   :   :	
Db	87	ENYFIKLVDVWVWYELQRDTCLSYSPLLQNMIDEFSDYYLSL-CKDTVSNKQLMAKLQESK	145
Qy	139	FDMVIVETFDYCPFLIAEKLKGFVAILSTSFSG-----SLEFGLPIPLSYVPVFRSLIT	192
		: : :             :               :	
Db	146	FDVLLSDPVAACGELIAEVLHIPFLYSLRFSPGYKIEKSSGRFIL--PPSYVPVILSGMG	203
Qy	193	DHMDFWGRVKNFL--MFFSFCRRQOHM--QSTFDNTIKEHFTEGSRPVLSHLLLKAELWF	248
		: :       :         : :     :	
Db	204	GPMTFIDRVKNMICTLYFDF--WFHMFNAKKWDPFYSEIF--GRPTTLAETMGKAEMWL	258
Qy	249	INSDFAFDFARPLLNTVYVGGGLEMEKPIKVPQDLENFIAKFGDSGFVLVTLGSMVNTCQ	308
		: :         :     :     :   :   :   :   :	
Db	259	IRSYWDLEFPHTLPNVVDYIGGLQCRPPKPLPKDMEFVQSSGEHGVVFSLGSMVSS--	316
Qy	309	NPEIFKEMNN----AFAHLPQGVIVKQCQSHWPKDVHLLAANVKIVDWLPQSDLLAHPSIR	364
		: :       :     :     :     :   :       : :	



Db 317 ---MTEEKANAIAWALAQIPQKVLWKFD---GKTPATLGPNTRVYKWLPQNDLLGHPKTK 370  
 Qy 365 LFVTHGGQNSIMEAIQHGVPMVGIPLEFGDQPENMVRVEAKKFGVSIQLKKLKAETLALKM 424  
 ||||| | : ||| ||:|||||:|:| :|: : || |:: :: : | :  
 Db 371 AFVTHGGANGVYEAIYHGIPMVGIPMFGEQHDNIAHMAVAKGAAVTLNIRTMSKTDLENAL 430  
 Qy 425 KQIMEDKRYKSAAVAASVILRSHPLSPTQRLVGWIDHVLQTGGATHLKPYVFQQPWHEQY 484  
 |:|: : || || | | |: | : | |: |: : || ||:| |:: :  
 Db 431 KEIINNPFYKKNVWLSTIHHDQPMKPLDKAVFWIEFVMRHKGAKHLRPLGHDLPWYQYH 490  
 Qy 485 LFDVVFVLL 493  
 || |||  
 Db 491 SLDVIGFLL 499

Search completed: May 7, 2004, 17:33:21  
 Job time : 22 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 7, 2004, 17:31:25 ; Search time 48 Seconds  
(without alignments)  
3024.321 Million cell updates/sec

Title: US-10-017-867A-282  
Perfect score: 2768  
Sequence: 1 MAGQRVLLLVGFLLPGVLLS.....GKLLGMAVWWLRGARKVKET 523

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1140673 seqs, 277566755 residues

Total number of hits satisfying chosen parameters: 1140673

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published\_Applications\_AA:\*  
1: /cgn2\_6/ptodata/2/pubpaa/US07\_PUBCOMB.pep:\*  
2: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep:\*  
3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep:\*  
4: /cgn2\_6/ptodata/2/pubpaa/US06\_PUBCOMB.pep:\*  
5: /cgn2\_6/ptodata/2/pubpaa/US07\_NEW\_PUB.pep:\*  
6: /cgn2\_6/ptodata/2/pubpaa/PCTUS\_PUBCOMB.pep:\*  
7: /cgn2\_6/ptodata/2/pubpaa/US08\_NEW\_PUB.pep:\*  
8: /cgn2\_6/ptodata/2/pubpaa/US08\_PUBCOMB.pep:\*  
9: /cgn2\_6/ptodata/2/pubpaa/US09A\_PUBCOMB.pep:\*  
10: /cgn2\_6/ptodata/2/pubpaa/US09B\_PUBCOMB.pep:\*  
11: /cgn2\_6/ptodata/2/pubpaa/US09C\_PUBCOMB.pep:\*  
12: /cgn2\_6/ptodata/2/pubpaa/US09\_NEW\_PUB.pep:\*  
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14: /cgn2\_6/ptodata/2/pubpaa/US10B\_PUBCOMB.pep:\*  
15: /cgn2\_6/ptodata/2/pubpaa/US10C\_PUBCOMB.pep:\*  
16: /cgn2\_6/ptodata/2/pubpaa/US10\_NEW\_PUB.pep:\*  
17: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep:\*  
18: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result	%	Query					
No.	Score	Match Length	DB	ID			Description

1	2768	100.0	523	10	US-09-946-374-282	Sequence 282, App
2	2768	100.0	523	12	US-10-006-485A-282	Sequence 282, App
3	2768	100.0	523	12	US-10-013-907A-282	Sequence 282, App
4	2768	100.0	523	12	US-10-015-499A-282	Sequence 282, App
5	2768	100.0	523	12	US-10-013-910A-282	Sequence 282, App
6	2768	100.0	523	12	US-10-226-254A-282	Sequence 282, App
7	2768	100.0	523	12	US-10-015-395A-282	Sequence 282, App
8	2768	100.0	523	14	US-10-006-856A-282	Sequence 282, App
9	2768	100.0	523	14	US-10-006-818A-282	Sequence 282, App
10	2768	100.0	523	14	US-10-015-393A-282	Sequence 282, App
11	2768	100.0	523	14	US-10-015-869A-282	Sequence 282, App
12	2768	100.0	523	14	US-10-012-121A-282	Sequence 282, App
13	2768	100.0	523	14	US-10-006-116A-282	Sequence 282, App
14	2768	100.0	523	14	US-10-006-117A-282	Sequence 282, App
15	2768	100.0	523	14	US-10-017-527A-282	Sequence 282, App
16	2768	100.0	523	14	US-10-013-913A-282	Sequence 282, App
17	2768	100.0	523	14	US-10-007-194A-282	Sequence 282, App
18	2768	100.0	523	14	US-10-013-430A-282	Sequence 282, App
19	2768	100.0	523	14	US-10-011-671A-282	Sequence 282, App
20	2768	100.0	523	14	US-10-012-755A-282	Sequence 282, App
21	2768	100.0	523	14	US-10-015-386A-282	Sequence 282, App
22	2768	100.0	523	14	US-10-011-692A-282	Sequence 282, App
23	2768	100.0	523	14	US-10-006-768A-282	Sequence 282, App
24	2768	100.0	523	14	US-10-017-610A-282	Sequence 282, App
25	2768	100.0	523	14	US-10-006-063A-282	Sequence 282, App
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27	2768	100.0	523	14	US-10-015-391A-282	Sequence 282, App
28	2768	100.0	523	14	US-10-017-407A-282	Sequence 282, App
29	2768	100.0	523	14	US-10-011-833A-282	Sequence 282, App
30	2768	100.0	523	14	US-10-006-041A-282	Sequence 282, App
31	2768	100.0	523	14	US-10-015-822A-282	Sequence 282, App
32	2768	100.0	523	14	US-10-015-387A-282	Sequence 282, App
33	2768	100.0	523	14	US-10-006-130A-282	Sequence 282, App
34	2768	100.0	523	14	US-10-006-172A-282	Sequence 282, App
35	2768	100.0	523	14	US-10-017-253A-282	Sequence 282, App
36	2768	100.0	523	14	US-10-015-392A-282	Sequence 282, App
37	2768	100.0	523	14	US-10-017-306A-282	Sequence 282, App
38	2768	100.0	523	14	US-10-017-867A-282	Sequence 282, App
39	2768	100.0	523	14	US-10-012-064A-282	Sequence 282, App
40	2768	100.0	523	14	US-10-013-909A-282	Sequence 282, App
41	2768	100.0	523	14	US-10-015-671A-282	Sequence 282, App
42	2768	100.0	523	14	US-10-015-610A-282	Sequence 282, App
43	2768	100.0	523	14	US-10-012-137A-282	Sequence 282, App
44	2768	100.0	523	14	US-10-012-752A-282	Sequence 282, App
45	2768	100.0	523	14	US-10-012-754A-282	Sequence 282, App

#### ALIGNMENTS

RESULT 1  
 US-09-946-374-282  
 ; Sequence 282, Application US/09946374  
 ; Publication No. US20030073129A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Baker, Kevin P.

; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, Christopher J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth J.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Smith, Victoria  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; TITLE OF INVENTION: Acids Encoding the Same  
; FILE REFERENCE: P2830P1C1  
; CURRENT APPLICATION NUMBER: US/09/946,374  
; CURRENT FILING DATE: 2001-09-04  
; PRIOR APPLICATION NUMBER: 60/098716  
; PRIOR FILING DATE: 1998-09-01  
; PRIOR APPLICATION NUMBER: 60/098723  
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; PRIOR APPLICATION NUMBER: 60/105693
; PRIOR FILING DATE: 1998-10-26
; PRIOR APPLICATION NUMBER: 60/105694
; PRIOR FILING DATE: 1998-10-26
; PRIOR APPLICATION NUMBER: 60/105807
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Query Match          100.0%; Score 2768; DB 10; Length 523;
Best Local Similarity 100.0%; Pred. No. 6.6e-272;
Matches 523; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy      1 MAGQRVLLLVGFLLPGVLLSEAAKILTISTVGGSHYLLMDRVSQILQDHGHNVTMLNHKR 60
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Db      1 MAGQRVLLLVGFLLPGVLLSEAAKILTISTVGGSHYLLMDRVSQILQDHGHNVTMLNHKR 60

Qy     61 GPFMPDFKKEEKSYQVISWLAPEDHQREFKKSFDFFLEETLGGRGKFENLLNVLEYLALQ 120
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Db     61 GPFMPDFKKEEKSYQVISWLAPEDHQREFKKSFDFFLEETLGGRGKFENLLNVLEYLALQ 120

Qy    121 CSHFLNRKDIMDSLKNENFDMVIVETFDYCPFLIAEKLGKPFVAILSTSFGSLEFGLPIP 180
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Db    121 CSHFLNRKDIMDSLKNENFDMVIVETFDYCPFLIAEKLGKPFVAILSTSFGSLEFGLPIP 180

Qy    181 LSYVPVFRSLTLDHMDFWGRVKNFLMFFSFCRRQQHMQSTFDNTIKEHFTEGSRPVLSHL 240
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Db    181 LSYVPVFRSLTLDHMDFWGRVKNFLMFFSFCRRQQHMQSTFDNTIKEHFTEGSRPVLSHL 240

Qy    241 LLKAELWFINSDFAFDFARPLLNTVYVGGLMEKPIKVPQDLENFIAKFGDSGFVLVTL 300
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Qy    301 GSMVNTCQNPEIFKEMNNAFAHLPQGVWKCQCCHWPKDVHLLAANVKIVDWLPQSDLLAH 360
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Qy    361 PSIRLFVTHGGQNSIMEAIQHGVPVMVGIPFLGDPENMVRVEAKKFGVSIQLKKLKAETL 420
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 Qy 481 HEQYLFDFVFVFLGLTLGTLWLCLCGKLLGMAVWWLRGARKVKET 523  
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RESULT 2

US-10-006-485A-282

; Sequence 282, Application US/10006485A  
 ; Publication No. US20030064062A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Baker, Kevin P.  
 ; APPLICANT: Botstein, David  
 ; APPLICANT: Desnoyers, Luc  
 ; APPLICANT: Eaton, Dan l.  
 ; APPLICANT: Ferrara, Napoleone  
 ; APPLICANT: Fong, Sherman  
 ; APPLICANT: Gao, Wei-Qiang  
 ; APPLICANT: Goddard, Audrey  
 ; APPLICANT: Godowski, Paul J.  
 ; APPLICANT: Grimaldi, Christopher J.  
 ; APPLICANT: Gurney, Austin L.  
 ; APPLICANT: Hillan, Kenneth J.  
 ; APPLICANT: Pan, James  
 ; APPLICANT: Paoni, Nicholas F.  
 ; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
 ; TITLE OF INVENTION: Acids Encoding the Same  
 ; FILE REFERENCE: P2830P1C9  
 ; CURRENT APPLICATION NUMBER: US/10/006,485A  
 ; CURRENT FILING DATE: 2001-12-06  
 ; PRIOR APPLICATION NUMBER: 60/098716  
 ; PRIOR FILING DATE: 1998-09-01  
 ; PRIOR APPLICATION NUMBER: 60/098723  
 ; PRIOR FILING DATE: 1998-09-01  
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 ; PRIOR APPLICATION NUMBER: 60/098803  
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; PRIOR FILING DATE: 1998-09-09  
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; PRIOR APPLICATION NUMBER: 60/100683  
; PRIOR FILING DATE: 1998-09-17  
; PRIOR APPLICATION NUMBER: 60/100684  
; PRIOR FILING DATE: 1998-09-17  
; PRIOR APPLICATION NUMBER: 60/100710  
; PRIOR FILING DATE: 1998-09-17  
; PRIOR APPLICATION NUMBER: 60/100711  
; PRIOR FILING DATE: 1998-09-17  
; PRIOR APPLICATION NUMBER: 60/100848  
; PRIOR FILING DATE: 1998-09-18  
; PRIOR APPLICATION NUMBER: 60/100849  
; PRIOR FILING DATE: 1998-09-18  
; PRIOR APPLICATION NUMBER: 60/100919  
; PRIOR FILING DATE: 1998-09-17  
; PRIOR APPLICATION NUMBER: 60/100930  
; PRIOR FILING DATE: 1998-09-17  
; PRIOR APPLICATION NUMBER: 60/101014  
; PRIOR FILING DATE: 1998-09-18  
; PRIOR APPLICATION NUMBER: 60/101068  
; PRIOR FILING DATE: 1998-09-18  
; PRIOR APPLICATION NUMBER: 60/101071  
; PRIOR FILING DATE: 1998-09-18  
; PRIOR APPLICATION NUMBER: 60/101279  
; PRIOR FILING DATE: 1998-09-22

; PRIOR APPLICATION NUMBER: 60/101471  
; PRIOR FILING DATE: 1998-09-23  
; PRIOR APPLICATION NUMBER: 60/101472  
; PRIOR FILING DATE: 1998-09-23  
; PRIOR APPLICATION NUMBER: 60/101474  
; PRIOR FILING DATE: 1998-09-23  
; PRIOR APPLICATION NUMBER: 60/101475  
; PRIOR FILING DATE: 1998-09-23  
; PRIOR APPLICATION NUMBER: 60/101476  
; PRIOR FILING DATE: 1998-09-23  
; PRIOR APPLICATION NUMBER: 60/101477  
; PRIOR FILING DATE: 1998-09-23  
; PRIOR APPLICATION NUMBER: 60/101479  
; PRIOR FILING DATE: 1998-09-23  
; PRIOR APPLICATION NUMBER: 60/101738  
; PRIOR FILING DATE: 1998-09-24  
; PRIOR APPLICATION NUMBER: 60/101741  
; PRIOR FILING DATE: 1998-09-24  
; PRIOR APPLICATION NUMBER: 60/101743  
; PRIOR FILING DATE: 1998-09-24  
; PRIOR APPLICATION NUMBER: 60/101915  
; PRIOR FILING DATE: 1998-09-24  
; PRIOR APPLICATION NUMBER: 60/101916  
; PRIOR FILING DATE: 1998-09-24  
; PRIOR APPLICATION NUMBER: 60/102207  
; PRIOR FILING DATE: 1998-09-29  
; PRIOR APPLICATION NUMBER: 60/102240  
; PRIOR FILING DATE: 1998-09-29  
; PRIOR APPLICATION NUMBER: 60/102307  
; PRIOR FILING DATE: 1998-09-29  
; PRIOR APPLICATION NUMBER: 60/102330  
; PRIOR FILING DATE: 1998-09-29  
; PRIOR APPLICATION NUMBER: 60/102331  
; PRIOR FILING DATE: 1998-09-29  
; PRIOR APPLICATION NUMBER: 60/102484  
; PRIOR FILING DATE: 1998-09-30  
; PRIOR APPLICATION NUMBER: 60/102487  
; PRIOR FILING DATE: 1998-09-30  
; PRIOR APPLICATION NUMBER: 60/102570  
; PRIOR FILING DATE: 1998-09-30  
; PRIOR APPLICATION NUMBER: 60/102571  
; PRIOR FILING DATE: 1998-09-30  
; PRIOR APPLICATION NUMBER: 60/102684  
; PRIOR FILING DATE: 1998-10-01  
; PRIOR APPLICATION NUMBER: 60/102687  
; PRIOR FILING DATE: 1998-10-01  
; PRIOR APPLICATION NUMBER: 60/102965  
; PRIOR FILING DATE: 1998-10-02  
; PRIOR APPLICATION NUMBER: 60/103258  
; PRIOR FILING DATE: 1998-10-06  
; PRIOR APPLICATION NUMBER: 60/103314  
; PRIOR FILING DATE: 1998-10-07  
; PRIOR APPLICATION NUMBER: 60/103315  
; PRIOR FILING DATE: 1998-10-07  
; PRIOR APPLICATION NUMBER: 60/103328  
; PRIOR FILING DATE: 1998-10-07  
; PRIOR APPLICATION NUMBER: 60/103395

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; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103396
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103401
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103449
; PRIOR FILING DATE: 1998-10-06
; PRIOR APPLICATION NUMBER: 60/103633
; PRIOR FILING DATE: 1998-10-08
; PRIOR APPLICATION NUMBER: 60/103678
; PRIOR FILING DATE: 1998-10-08
; PRIOR APPLICATION NUMBER: 60/103679
; PRIOR FILING DATE: 1998-10-08
; PRIOR APPLICATION NUMBER: 60/103711
; PRIOR FILING DATE: 1998-10-08
; PRIOR APPLICATION NUMBER: 60/104257
; PRIOR FILING DATE: 1998-10-14
; PRIOR APPLICATION NUMBER: 60/104987
; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: 60/105000
; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: 60/105002
; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: 60/105104
; PRIOR FILING DATE: 1998-10-21
; PRIOR APPLICATION NUMBER: 60/105169
; PRIOR FILING DATE: 1998-10-22
; PRIOR APPLICATION NUMBER: 60/105266
; PRIOR FILING DATE: 1998-10-22
; PRIOR APPLICATION NUMBER: 60/105693
; PRIOR FILING DATE: 1998-10-26
; PRIOR APPLICATION NUMBER: 60/105694
; PRIOR FILING DATE: 1998-10-26
; PRIOR APPLICATION NUMBER: 60/105807
; PRIOR FILING DATE: 1998-10-27
; PRIOR APPLICATION NUMBER: 60/105881
; PRIOR FILING DATE: 1998-10-27
; PRIOR APPLICATION NUMBER: 60/105882
; PRIOR FILING DATE: 1998-10-27
; PRIOR APPLICATION NUMBER: 60/106023
; PRIOR FILING DATE: 1998-10-28

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Query Match          100.0%; Score 2768; DB 12; Length 523;
Best Local Similarity 100.0%; Pred. No. 6.6e-272;
Matches 523; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 MAGQRVLLLVGFLLPGVLLSEAAKILTISTVGGSHYLLMDRVSQILQDHGHNVTMLNHKR 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MAGQRVLLLVGFLLPGVLLSEAAKILTISTVGGSHYLLMDRVSQILQDHGHNVTMLNHKR 60

Qy     61 GPFMPDFKKEEKSQVISWLAPEDHQREFKKSFDFFLEETLGGRGKFENLLNVLEYLALQ 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 GPFMPDFKKEEKSQVISWLAPEDHQREFKKSFDFFLEETLGGRGKFENLLNVLEYLALQ 120

Qy    121 CSHFLNRKDIMDSLKNENFDMVIVETFDYCPFLIAEKLGKPFVAILSTSFGSLEFGLPIP 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 CSHFLNRKDIMDSLKNENFDMVIVETFDYCPFLIAEKLGKPFVAILSTSFGSLEFGLPIP 180

```

Qy 181 LSYVPVFRSLTDMDFWGRVKNFLMFFSFCRRQQHMQSTFDNTIKEHFTEGSRPVLSHL 240  
 |||  
 Db 181 LSYVPVFRSLTDMDFWGRVKNFLMFFSFCRRQQHMQSTFDNTIKEHFTEGSRPVLSHL 240

Qy 241 LLKAELWFINSDFAFDFARPLLNTVYVGGLMEKPIKVPQDLENFIAKFGDSGFVLVTL 300  
 |||  
 Db 241 LLKAELWFINSDFAFDFARPLLNTVYVGGLMEKPIKVPQDLENFIAKFGDSGFVLVTL 300

Qy 301 GSMVNTCQNPEIFKEMNNAFAHLPQGVWKCQC SHWPKDVHLAANVKIVDWLPQSDLLAH 360  
 |||  
 Db 301 GSMVNTCQNPEIFKEMNNAFAHLPQGVWKCQC SHWPKDVHLAANVKIVDWLPQSDLLAH 360

Qy 361 PSIRLFVTHGGQNSIMEAIQHGVPMVGIPLEFGDQPENMVRVEAKKFGVSIQLKKLKAETL 420  
 |||  
 Db 361 PSIRLFVTHGGQNSIMEAIQHGVPMVGIPLEFGDQPENMVRVEAKKFGVSIQLKKLKAETL 420

Qy 421 ALKMKQIMEDKRYKSAAVAASVILRSHPLSPTQRLVGWIDHVLQTGGATHLKPYVFQQPW 480  
 |||  
 Db 421 ALKMKQIMEDKRYKSAAVAASVILRSHPLSPTQRLVGWIDHVLQTGGATHLKPYVFQQPW 480

Qy 481 HEQYLFDFVFLGLTLGLTLWLCLCGKLLGMAVWWLRGARKVKET 523  
 |||  
 Db 481 HEQYLFDFVFLGLTLGLTLWLCLCGKLLGMAVWWLRGARKVKET 523

RESULT 3

US-10-013-907A-282

; Sequence 282, Application US/10013907A

; Publication No. US20030064925A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.

; APPLICANT: Botstein, David

; APPLICANT: Desnoyers, Luc

; APPLICANT: Eaton, Dan l.

; APPLICANT: Ferrara, Napoleone

; APPLICANT: Fong, Sherman

; APPLICANT: Gao, Wei-Qiang

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Grimaldi, Christopher J.

; APPLICANT: Gurney, Austin L.

; APPLICANT: Hillan, Kenneth J.

; APPLICANT: Pan, James

; APPLICANT: Paoni, Nicholas F.

; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

; TITLE OF INVENTION: Acids Encoding the Same

; FILE REFERENCE: P2830P1C34

; CURRENT APPLICATION NUMBER: US/10/013,907A

; CURRENT FILING DATE: 2001-12-10

; Prior Application removed - See File Wrapper or Palm

; NUMBER OF SEQ ID NOS: 477

; SEQ ID NO 282

; LENGTH: 523

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-013-907A-282

Query Match 100.0%; Score 2768; DB 12; Length 523;  
 Best Local Similarity 100.0%; Pred. No. 6.6e-272;  
 Matches 523; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 MAGQRVLLLVGFLLPGVLLSEAAKILTISTVGGSHYLLMDRVSQILQDHGHNVTMLNHKR 60
        |
Db      1 MAGQRVLLLVGFLLPGVLLSEAAKILTISTVGGSHYLLMDRVSQILQDHGHNVTMLNHKR 60

Qy     61 GPFMPDFKKKEEKSYQVISWLAPEDHQREFKKSFDFFLEETLGGRGKFENLLNVLEYLALQ 120
        |
Db     61 GPFMPDFKKKEEKSYQVISWLAPEDHQREFKKSFDFFLEETLGGRGKFENLLNVLEYLALQ 120

Qy    121 CSHFLNRKDIMDSLKNENFDMVIVETFDYCPFLIAEKLKGPFFVAILSTSFGSLEFGLPIP 180
        |
Db    121 CSHFLNRKDIMDSLKNENFDMVIVETFDYCPFLIAEKLKGPFFVAILSTSFGSLEFGLPIP 180

Qy    181 LSYVPVFRSLLTDHMDFWGRVKNFLMFFSFCCRQQHMQSTFDNTIKEHFTEGSRPVLSHL 240
        |
Db    181 LSYVPVFRSLLTDHMDFWGRVKNFLMFFSFCCRQQHMQSTFDNTIKEHFTEGSRPVLSHL 240

Qy    241 LLKAELWFINSDFAFDFARPLLNTVYVGGLMKPKPKVPQDLENFIAKFGDSGFVLVTL 300
        |
Db    241 LLKAELWFINSDFAFDFARPLLNTVYVGGLMKPKPKVPQDLENFIAKFGDSGFVLVTL 300

Qy    301 GSMVNTCQNPEIFKEMNNAFAHLPQGVIWKCQCCHWPKDVHLAANVKIVDWLPQSDLLAH 360
        |
Db    301 GSMVNTCQNPEIFKEMNNAFAHLPQGVIWKCQCCHWPKDVHLAANVKIVDWLPQSDLLAH 360

Qy    361 PSIRLFVTHGGQNSIMEAIQHGVPVVGIPPLFGDQPENMVRVEAKKFGVSIQLKKLKAETL 420
        |
Db    361 PSIRLFVTHGGQNSIMEAIQHGVPVVGIPPLFGDQPENMVRVEAKKFGVSIQLKKLKAETL 420

Qy    421 ALKMKQIMEDKRYKSAAVAASVILRSHPLSPTQRLVGWIDHVLQTGGATHLKPYVFQQPW 480
        |
Db    421 ALKMKQIMEDKRYKSAAVAASVILRSHPLSPTQRLVGWIDHVLQTGGATHLKPYVFQQPW 480

Qy    481 HEQYLFDFVFVFLGLTLGTLWLWLCGKLLGMAVWWLRGARKVKET 523
        |
Db    481 HEQYLFDFVFVFLGLTLGTLWLWLCGKLLGMAVWWLRGARKVKET 523
  
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#### RESULT 4

US-10-015-499A-282

; Sequence 282, Application US/10015499A

; Publication No. US20030065142A1

#### ; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.

; APPLICANT: Botstein, David

; APPLICANT: Desnoyers, Luc

; APPLICANT: Eaton, Dan l.

; APPLICANT: Ferrara, Napoleone

; APPLICANT: Fong, Sherman

; APPLICANT: Gao, Wei-Qiang

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Grimaldi, Christopher J.

```

; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830P1C42
; CURRENT APPLICATION NUMBER: US/10/015,499A
; CURRENT FILING DATE: 2001-12-11
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 282
; LENGTH: 523
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-015-499A-282

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Query Match          100.0%; Score 2768; DB 12; Length 523;
Best Local Similarity 100.0%; Pred. No. 6.6e-272;
Matches 523; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 MAGQRVLLLVGFLLPGVLLSEAAKILTISTVGGSHYLLMDRVSQILQDHGHNVTMLNHR 60
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MAGQRVLLLVGFLLPGVLLSEAAKILTISTVGGSHYLLMDRVSQILQDHGHNVTMLNHR 60

Qy     61 GPFMPDFKKEEKSYQVISWLAPEDHQREFKKSFDFFLEETLGGRGKFENLLNVLEYLALQ 120
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 GPFMPDFKKEEKSYQVISWLAPEDHQREFKKSFDFFLEETLGGRGKFENLLNVLEYLALQ 120

Qy    121 CSHFLNRKDIMDSLKNENFDMVIVETFDYCPFLIAEKLKGKPFVAILSTSFGSLEFGLPIP 180
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 CSHFLNRKDIMDSLKNENFDMVIVETFDYCPFLIAEKLKGKPFVAILSTSFGSLEFGLPIP 180

Qy    181 LSYVPVFRSLLTDHMDFWGRVKNFLMFFSFCRRQQHMQSTFDNTIKEHFTEGSRPVLSHL 240
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 LSYVPVFRSLLTDHMDFWGRVKNFLMFFSFCRRQQHMQSTFDNTIKEHFTEGSRPVLSHL 240

Qy    241 LLKAELWFINSDFAFDFARPLLENTVYVGGIMEKPIKVPQDLENFIAKFGDSGFVLVTL 300
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 LLKAELWFINSDFAFDFARPLLENTVYVGGIMEKPIKVPQDLENFIAKFGDSGFVLVTL 300

Qy    301 GSMVNTCQNPEIFKEMNNAFAHLPQGVWKQCQSHWPKDVHLAANVKIVDWLPQSDLLAH 360
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 GSMVNTCQNPEIFKEMNNAFAHLPQGVWKQCQSHWPKDVHLAANVKIVDWLPQSDLLAH 360

Qy    361 PSIRLFVTHGGQNSIMEAIQHGVPMVGIPFGDQPENMVRVEAKKFGVSIQLKKLKAETL 420
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 PSIRLFVTHGGQNSIMEAIQHGVPMVGIPFGDQPENMVRVEAKKFGVSIQLKKLKAETL 420

Qy    421 ALKMKQIMEDKRYKSAAVAASVILRSHPLSPTQRLVGWIDHVLQTTGGATHLKPYVFQQPW 480
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 ALKMKQIMEDKRYKSAAVAASVILRSHPLSPTQRLVGWIDHVLQTTGGATHLKPYVFQQPW 480

Qy    481 HEQYLFDFVFVFLGLTLGTLWLCLGKLLGMAVWWLRGARKVKET 523
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 HEQYLFDFVFVFLGLTLGTLWLCLGKLLGMAVWWLRGARKVKET 523

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RESULT 5

US-10-013-910A-282

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; Sequence 282, Application US/10013910A
; Publication No. US20030187192A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan l.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830P1C33
; CURRENT APPLICATION NUMBER: US/10/013,910A
; CURRENT FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: 60/098716
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098723
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098749
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098750
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098803
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/098821
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/098843
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/099536
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099596
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099598
; PRIOR FILING DATE: 1998-09-09
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 282
; LENGTH: 523
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-013-910A-282
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Query Match          100.0%; Score 2768; DB 12; Length 523;
Best Local Similarity 100.0%; Pred. No. 6.6e-272;
Matches 523; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy	1	MAGQRVLLLVGFLLPGVLLSEAAKILTISTVGGSHYLLMDRVSQILQDHGHNVTMLNHKR	60
Db	1	MAGQRVLLLVGFLLPGVLLSEAAKILTISTVGGSHYLLMDRVSQILQDHGHNVTMLNHKR	60
Qy	61	GPFMPDFKKEEKSYQVISWLPEDHQREFKKSFDFFLEETLGGRGKFENLLNVLEYLALQ	120
Db	61	GPFMPDFKKEEKSYQVISWLPEDHQREFKKSFDFFLEETLGGRGKFENLLNVLEYLALQ	120
Qy	121	CSHFLNRKDIMDSLKNENFDMVIVETFDCPFLIAEKLKGKPFVAILSTSFSGSLEFGLPIP	180
Db	121	CSHFLNRKDIMDSLKNENFDMVIVETFDCPFLIAEKLKGKPFVAILSTSFSGSLEFGLPIP	180
Qy	181	LSYVPVFRSLLTDHMDFWGRVKNFLMFFSFCRRQOHMQSTFDNTIKEHFTEGSRPVLSHL	240
Db	181	LSYVPVFRSLLTDHMDFWGRVKNFLMFFSFCRRQOHMQSTFDNTIKEHFTEGSRPVLSHL	240
Qy	241	LLKAELWFINSDFAFDFARPLLNTVYVGGLMEKPIKVPQDLENFIAKFGDSGFVLVTL	300
Db	241	LLKAELWFINSDFAFDFARPLLNTVYVGGLMEKPIKVPQDLENFIAKFGDSGFVLVTL	300
Qy	301	GSMVNTCQNPEIFKEMNNAFAHLPQGVWKCQC SHWPKDVHLAANVKIVDWLPQSDLLAH	360
Db	301	GSMVNTCQNPEIFKEMNNAFAHLPQGVWKCQC SHWPKDVHLAANVKIVDWLPQSDLLAH	360
Qy	361	PSIRLFVTHGGQNSIMEAIQHGVPMVGIPLEFGDQPENMVRVEAKKFGVSIQLKKLKAETL	420
Db	361	PSIRLFVTHGGQNSIMEAIQHGVPMVGIPLEFGDQPENMVRVEAKKFGVSIQLKKLKAETL	420
Qy	421	ALKMKQIMEDKRYKSAAVAASVILRSHPLSPTQRLVGWIDHVLQTTGGATHLKPYVFQQPW	480
Db	421	ALKMKQIMEDKRYKSAAVAASVILRSHPLSPTQRLVGWIDHVLQTTGGATHLKPYVFQQPW	480
Qy	481	HEQYLFDFVFVLLGLTLGLTLWLCGKLLGMAVWWLRGARKVKET	523
Db	481	HEQYLFDFVFVLLGLTLGLTLWLCGKLLGMAVWWLRGARKVKET	523

RESULT 6

US-10-226-254A-282

; Sequence 282, Application US/10226254A

; Publication No. US20030224478A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.

; APPLICANT: Botstein, David

; APPLICANT: Desnoyers, Luc

; APPLICANT: Eaton, Dan I.

; APPLICANT: Ferrara, Napoleone

; APPLICANT: Fong, Sherman

; APPLICANT: Gao, Wei-Qiang

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Grimaldi, Christopher J.

; APPLICANT: Gurney, Austin L.

; APPLICANT: Hillan, Kenneth J.

; APPLICANT: Pan, James

; APPLICANT: Paoni, Nicholas F.

; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic



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; TITLE OF INVENTION:  Acids Encoding the Same
; FILE REFERENCE: P2830P1C68
; CURRENT APPLICATION NUMBER: US/10/226,254A
; CURRENT FILING DATE:  2002-08-21
; PRIOR APPLICATION NUMBER: 60/098716
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098723
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098749
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098750
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098803
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/098821
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/098843
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/099536
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099596
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099598
; PRIOR FILING DATE: 1998-09-09
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 282
;   LENGTH: 523
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-226-254A-282
```

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Query Match          100.0%;  Score 2768;  DB 12;  Length 523;
Best Local Similarity 100.0%;  Pred. No. 6.6e-272;
Matches 523;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;
```

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Qy      1 MAGQRVLLLVGFLLPGVLLSEAAKILTISTVGGSHYLLMDRVSQILQDHGHNVTMLNHKR 60
        |||
Db      1 MAGQRVLLLVGFLLPGVLLSEAAKILTISTVGGSHYLLMDRVSQILQDHGHNVTMLNHKR 60

Qy     61 GPFMPDFKKEEKSYQVISWLAPEDHQREFKKSFDFFLEETLGGRGKFENLLNVLEYLALQ 120
        |||
Db     61 GPFMPDFKKEEKSYQVISWLAPEDHQREFKKSFDFFLEETLGGRGKFENLLNVLEYLALQ 120

Qy    121 CSHFLNRKDIMDSLKNENFDMVIVETFDYCPFLIAEKLKGPVAILSTSFGSLEFGLPIP 180
        |||
Db    121 CSHFLNRKDIMDSLKNENFDMVIVETFDYCPFLIAEKLKGPVAILSTSFGSLEFGLPIP 180

Qy    181 LSYVPVFRSLLTDHMDFWGRVKNFLMFFSFCRRQQHMQSTFDNTIKEHFTEGSRPVLSHL 240
        |||
Db    181 LSYVPVFRSLLTDHMDFWGRVKNFLMFFSFCRRQQHMQSTFDNTIKEHFTEGSRPVLSHL 240

Qy    241 LLKAELWFINSDFAFDFARPLLNPNTVYVGGLMEKPIKVPQDLENFIAKFGDSGFVLVTL 300
        |||
Db    241 LLKAELWFINSDFAFDFARPLLNPNTVYVGGLMEKPIKVPQDLENFIAKFGDSGFVLVTL 300

Qy    301 GSMVNTCQNPEIFKEMNNAFAHLPGQVIWKCQCSHWPKDVHLAANVKIVDWLPQSDLLAH 360
```

```

Db      301 GSMVNTCQNPEIFKEMNNAFAHLPQGVIWKQCSEHWPKDVHLAANVKIVDWLPQSDLLAH 360
Qy      361 PSIRLFVTHGGQNSIMEAIQHGVPMVGIPLEFGDQPENMVRVEAKKFGVSIQLKKLKAETL 420
Db      361 PSIRLFVTHGGQNSIMEAIQHGVPMVGIPLEFGDQPENMVRVEAKKFGVSIQLKKLKAETL 420
Qy      421 ALKMKQIMEDKRYKSAAVAASVILRSHPLSPTQRLVGWIDHVLQTTGGATHLKPYVFQQPW 480
Db      421 ALKMKQIMEDKRYKSAAVAASVILRSHPLSPTQRLVGWIDHVLQTTGGATHLKPYVFQQPW 480
Qy      481 HEQYLFDFVVFLLGLTLGLTLWLCGKLLGMAVWWLRGARKVKET 523
Db      481 HEQYLFDFVVFLLGLTLGLTLWLCGKLLGMAVWWLRGARKVKET 523

```

# RESULT 7

US-10-015-395A-282

; Sequence 282, Application US/10015395A

; Publication No. US20040073015A1

## ; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.

; APPLICANT: Botstein, David

; APPLICANT: Desnoyers, Luc

; APPLICANT: Eaton, Dan I.

; APPLICANT: Ferrara, Napoleone

; APPLICANT: Fong, Sherman

; APPLICANT: Gao, Wei-Qiang

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Grimaldi, Christopher J.

; APPLICANT: Gurney, Austin L.

; APPLICANT: Hillan, Kenneth J.

; APPLICANT: Pan, James

; APPLICANT: Paoni, Nicholas F.

; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

; TITLE OF INVENTION: Acids Encoding the Same

; FILE REFERENCE: P2830P1C57

; CURRENT APPLICATION NUMBER: US/10/015,395A

; CURRENT FILING DATE: 2001-12-12

; Prior application removed - See file Wrapper or Palm

; NUMBER OF SEQ ID NOS: 477

; SEQ ID NO 282

; LENGTH: 523

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-015-395A-282

Query Match 100.0%; Score 2768; DB 12; Length 523;

Best Local Similarity 100.0%; Pred. No. 6.6e-272;

Matches 523; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

Qy      1 MAGQRVLLLVGFLLPGVLLSEAAKILTISTVGGSHYLLMDRVSQILQDHGHNVMTLNHKR 60
Db      1 MAGQRVLLLVGFLLPGVLLSEAAKILTISTVGGSHYLLMDRVSQILQDHGHNVMTLNHKR 60
Qy      61 GPFMPDFKKEEKSYQVISWLAPEDHQREFKKSFDFFLEETLGGRGKFENLLNVLEYLALQ 120

```

Db	61	GPFPDPFKKEEKSYQVISWLAPEDHQREFKKSFDFFLEETLGGRGKFENLLNVLEYLALQ	120
Qy	121	CSHFLNRKDIMDSLKNENFDMVIVETFDYCPFLIAEKLGKPFVAILSTSFGSLEFGLPIP	180
Db	121	CSHFLNRKDIMDSLKNENFDMVIVETFDYCPFLIAEKLGKPFVAILSTSFGSLEFGLPIP	180
Qy	181	LSYVPVFRSLLTDHMDFWGRVKNFLMFFSFCRRQQHMQSTFDNTIKEHFTEGSRPVLSHL	240
Db	181	LSYVPVFRSLLTDHMDFWGRVKNFLMFFSFCRRQQHMQSTFDNTIKEHFTEGSRPVLSHL	240
Qy	241	LLKAELWFINSDFAFDFARPLLNTVYVGGLMEKPIKVPQDLENFIAKFGDSGFVLVTL	300
Db	241	LLKAELWFINSDFAFDFARPLLNTVYVGGLMEKPIKVPQDLENFIAKFGDSGFVLVTL	300
Qy	301	GSMVNTCQNPEIFKEMNNAFAHLPQGVIWKQCQSHWPKDVHLAANVKIVDWLPQSDLLAH	360
Db	301	GSMVNTCQNPEIFKEMNNAFAHLPQGVIWKQCQSHWPKDVHLAANVKIVDWLPQSDLLAH	360
Qy	361	PSIRLFVTHGGQNSIMEAIQHGVPMVGIPLFGDQPENMVRVEAKKFGVSIQLKKLKAETL	420
Db	361	PSIRLFVTHGGQNSIMEAIQHGVPMVGIPLFGDQPENMVRVEAKKFGVSIQLKKLKAETL	420
Qy	421	ALKMKQIMEDKRYKSAAVAASVILRSHPLSPTQRLVGWIDHVLQTGGATHLKPYVFQQPW	480
Db	421	ALKMKQIMEDKRYKSAAVAASVILRSHPLSPTQRLVGWIDHVLQTGGATHLKPYVFQQPW	480
Qy	481	HEQYLFDFVVFLLGLTLGTLWLWLCGKLLGMAVWWLRGARKVKET	523
Db	481	HEQYLFDFVVFLLGLTLGTLWLWLCGKLLGMAVWWLRGARKVKET	523

RESULT 8

US-10-006-856A-282

; Sequence 282, Application US/10006856A

; Publication No. US20030044841A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.

; APPLICANT: Botstein, David

; APPLICANT: Desnoyers, Luc

; APPLICANT: Eaton, Dan l.

; APPLICANT: Ferrara, Napoleone

; APPLICANT: Fong, Sherman

; APPLICANT: Gao, Wei-Qiang

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Grimaldi, Christopher J.

; APPLICANT: Gurney, Austin L.

; APPLICANT: Hillan, Kenneth J.

; APPLICANT: Pan, James

; APPLICANT: Paoni, Nicholas F.

; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

; TITLE OF INVENTION: Acids Encoding the Same

; FILE REFERENCE: P2830P1C14

; CURRENT APPLICATION NUMBER: US/10/006,856A

; CURRENT FILING DATE: 2002-05-10

; NUMBER OF SEQ ID NOS: 477



; APPLICANT: Ferrara, Napoleone  
 ; APPLICANT: Fong, Sherman  
 ; APPLICANT: Gao, Wei-Qiang  
 ; APPLICANT: Goddard, Audrey  
 ; APPLICANT: Godowski, Paul J.  
 ; APPLICANT: Grimaldi, Christopher J.  
 ; APPLICANT: Gurney, Austin L.  
 ; APPLICANT: Hillan, Kenneth J.  
 ; APPLICANT: Pan, James  
 ; APPLICANT: Paoni, Nicholas F.  
 ; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
 ; TITLE OF INVENTION: Acids Encoding the Same  
 ; FILE REFERENCE: P2830P1C4  
 ; CURRENT APPLICATION NUMBER: US/10/006,818A  
 ; CURRENT FILING DATE: 2001-12-06  
 ; Prior Application removed - See File Wrapper or Palm  
 ; NUMBER OF SEQ ID NOS: 477  
 ; SEQ ID NO 282  
 ; LENGTH: 523  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-10-006-818A-282

Query Match 100.0%; Score 2768; DB 14; Length 523;  
 Best Local Similarity 100.0%; Pred. No. 6.6e-272;  
 Matches 523; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MAGQRVLLLVGFLLPGVLLSEAAKILTISTVGGSHYLLMDRVSQILQDHGHNVMTLNHKR	60
Db	1	MAGQRVLLLVGFLLPGVLLSEAAKILTISTVGGSHYLLMDRVSQILQDHGHNVMTLNHKR	60
Qy	61	GPFMPDFKKEEKSYQVISWLAPEDHQREFKKSFDFFLEETLGGRGKFENLLNVLEYLALQ	120
Db	61	GPFMPDFKKEEKSYQVISWLAPEDHQREFKKSFDFFLEETLGGRGKFENLLNVLEYLALQ	120
Qy	121	CSHFLNRKDIMDSLKNENFDMVIVETFDYCPFLIAEKLGKPFVAILSTSFGSLEFGLPIP	180
Db	121	CSHFLNRKDIMDSLKNENFDMVIVETFDYCPFLIAEKLGKPFVAILSTSFGSLEFGLPIP	180
Qy	181	LSYVPVFRSLLTDHMDFWGRVKNFLMFFSFCRRQQHMQSTFDNTIKEHFTEGSRPVLSHL	240
Db	181	LSYVPVFRSLLTDHMDFWGRVKNFLMFFSFCRRQQHMQSTFDNTIKEHFTEGSRPVLSHL	240
Qy	241	LLKAELWFINSDFAFDFARPLLNPNTVYVGGLMEKPIKPVPQDLENFIAKFGDSGFVLVTL	300
Db	241	LLKAELWFINSDFAFDFARPLLNPNTVYVGGLMEKPIKPVPQDLENFIAKFGDSGFVLVTL	300
Qy	301	GSMVNTCQNPEIFKEMNNAFAHLPGQVIWKCQCSHWPKDVHLAANVKIVDWLPQSDLLAH	360
Db	301	GSMVNTCQNPEIFKEMNNAFAHLPGQVIWKCQCSHWPKDVHLAANVKIVDWLPQSDLLAH	360
Qy	361	PSIRLFVTHGGQNSIMEAIQHGVPMVGIPLFGDQPENMVRVEAKKFGVSIQLKKLKAETL	420
Db	361	PSIRLFVTHGGQNSIMEAIQHGVPMVGIPLFGDQPENMVRVEAKKFGVSIQLKKLKAETL	420
Qy	421	ALKMKQIMEDKRYKSAVAASVILRSHPLSPTQRLVGWIDHVLQTGGATHLKPYPVQQPW	480

Db 421 ALKMKQIMEDKRYKSAAVAASVILRSHPLSPTQRLVGWIDHVLQTTGGATHLKPVVFQQPW 480  
Qy 481 HEQYLFDFVFVFLGLTLGLTLWLCLGKLLGMAVWWLRGARKVKET 523  
|||||  
Db 481 HEQYLFDFVFVFLGLTLGLTLWLCLGKLLGMAVWWLRGARKVKET 523

RESULT 10

US-10-015-393A-282

; Sequence 282, Application US/10015393A  
; Publication No. US20030069179A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan l.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, Christopher J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth J.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; TITLE OF INVENTION: Acids Encoding the Same  
; FILE REFERENCE: P2830P1C46  
; CURRENT APPLICATION NUMBER: US/10/015,393A  
; CURRENT FILING DATE: 2002-06-10  
; Prior Application removed - See File Wrapper or Palm  
; NUMBER OF SEQ ID NOS: 477  
; SEQ ID NO 282  
; LENGTH: 523  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-015-393A-282

Query Match 100.0%; Score 2768; DB 14; Length 523;  
Best Local Similarity 100.0%; Pred. No. 6.6e-272;  
Matches 523; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAGQRVLLLVGFLLPGVLLSEAAKILTISTVGGSHYLLMDRVSQILQDHGHNVTMLNHKR 60  
|||||  
Db 1 MAGQRVLLLVGFLLPGVLLSEAAKILTISTVGGSHYLLMDRVSQILQDHGHNVTMLNHKR 60  
  
Qy 61 GPFMPDFKKEEKSYQVISWLAPEDHQREFKKSFDFFLEETLGGRGKFENLLNVLEYLALQ 120  
|||||  
Db 61 GPFMPDFKKEEKSYQVISWLAPEDHQREFKKSFDFFLEETLGGRGKFENLLNVLEYLALQ 120  
  
Qy 121 CSHFLNRKDIMDSLKNENFDMVIVETFDYCPFLIAEKLKGKPFVAILSTSFGSLEFGLPIP 180  
|||||  
Db 121 CSHFLNRKDIMDSLKNENFDMVIVETFDYCPFLIAEKLKGKPFVAILSTSFGSLEFGLPIP 180  
  
Qy 181 LSYVPVFRSLLTDHMDFWGRVKNFLMFFSFCRRQQHMQSTFDNTIKEHFTGSRPVLSHL 240  
|||||

Db 181 LSYVPVFRSLLTDHMDFWGRVKNFLMFFSFCRRQQHMQSTFDNTIKEHFTEGSRPVLSHL 240

Qy 241 LLKAELWFINSDFAFDFARPLLNTVYVGGLMEKPIKPVPQDLENFIAKFGDSGFVLVTL 300  
 |||

Db 241 LLKAELWFINSDFAFDFARPLLNTVYVGGLMEKPIKPVPQDLENFIAKFGDSGFVLVTL 300

Qy 301 GSMVNTCQNPEIFKEMNNAFAHLPGQVIWKCQCShwPKDVHLAANVKIVDWLPQSDLLAH 360  
 |||

Db 301 GSMVNTCQNPEIFKEMNNAFAHLPGQVIWKCQCShwPKDVHLAANVKIVDWLPQSDLLAH 360

Qy 361 PSIRLFVTHGGQNSIMEAIQHGVPMVGIPFLGDQPENMVRVEAKKFGVSIQLKKLKAETL 420  
 |||

Db 361 PSIRLFVTHGGQNSIMEAIQHGVPMVGIPFLGDQPENMVRVEAKKFGVSIQLKKLKAETL 420

Qy 421 ALKMKQIMEDKRYKSAAVAASVILRSHPLSPTQRLVGWIDHVLQTGGATHLKPYPVQQPW 480  
 |||

Db 421 ALKMKQIMEDKRYKSAAVAASVILRSHPLSPTQRLVGWIDHVLQTGGATHLKPYPVQQPW 480

Qy 481 HEQYLFVDVVFLLGLTLGLTLWLCGKLLGMAVWWLRGARKVKET 523  
 |||

Db 481 HEQYLFVDVVFLLGLTLGLTLWLCGKLLGMAVWWLRGARKVKET 523

RESULT 11

US-10-015-869A-282

; Sequence 282, Application US/10015869A

; Publication No. US20030073130A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.

; APPLICANT: Botstein, David

; APPLICANT: Desnoyers, Luc

; APPLICANT: Eaton, Dan I.

; APPLICANT: Ferrara, Napoleone

; APPLICANT: Fong, Sherman

; APPLICANT: Gao, Wei-Qiang

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Grimaldi, Christopher J.

; APPLICANT: Gurney, Austin I.

; APPLICANT: Hillan, Kenneth J.

; APPLICANT: Pan, James

; APPLICANT: Paoni, Nicholas F.

; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

; TITLE OF INVENTION: Acids Encoding the Same

; FILE REFERENCE: P2830P1C45

; CURRENT APPLICATION NUMBER: US/10/015,869A

; CURRENT FILING DATE: 2002-06-25

; Prior Application removed - See File Wrapper or Palm

; NUMBER OF SEQ ID NOS: 477

; SEQ ID NO 282

; LENGTH: 523

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-015-869A-282

Query Match 100.0%; Score 2768; DB 14; Length 523;

Best Local Similarity 100.0%; Pred. No. 6.6e-272;

Matches 523; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

Qy      1 MAGQRVLLLVGFLLPGVLLSEAAKILTISTVGGSHYLLMDRVSQILQDHGHNVTMLNHKR 60
      |||
Db      1 MAGQRVLLLVGFLLPGVLLSEAAKILTISTVGGSHYLLMDRVSQILQDHGHNVTMLNHKR 60

Qy     61 GPFMPDFKKEEKSYQVISWLAPEDHQREFKKSFDFFLEETLGGRGKFENLLNVLEYLALQ 120
      |||
Db     61 GPFMPDFKKEEKSYQVISWLAPEDHQREFKKSFDFFLEETLGGRGKFENLLNVLEYLALQ 120

Qy    121 CSHFLNRKDIMDSLKNENFDMVIVETFDYCPFLIAEKLGKPFVAILSTSFGSLEFGLPIP 180
      |||
Db    121 CSHFLNRKDIMDSLKNENFDMVIVETFDYCPFLIAEKLGKPFVAILSTSFGSLEFGLPIP 180

Qy    181 LSYVPVFRSLLTDHMDFWGRVKNFLMFFSFCRRQQHMQSTFDNTIKEHFTEGSRPVLSHL 240
      |||
Db    181 LSYVPVFRSLLTDHMDFWGRVKNFLMFFSFCRRQQHMQSTFDNTIKEHFTEGSRPVLSHL 240

Qy    241 LLKAELWFINSDFAFDFAFARPLLNTVYVGGLMEKPIKPVPQDLENFIAKFGDSGFVLVTL 300
      |||
Db    241 LLKAELWFINSDFAFDFAFARPLLNTVYVGGLMEKPIKPVPQDLENFIAKFGDSGFVLVTL 300

Qy   301 GSMVNTCQNPEIFKEMNNAFAHLPOGVIWKCQCShwPKDVHLAANVKIVDWLPQSDLLAH 360
      |||
Db   301 GSMVNTCQNPEIFKEMNNAFAHLPOGVIWKCQCShwPKDVHLAANVKIVDWLPQSDLLAH 360

Qy   361 PSIRLFVTHGGQNSIMEAIQHGVPMVGIPFGDQPENMVRVEAKKFGVSIQLKKLKAETL 420
      |||
Db   361 PSIRLFVTHGGQNSIMEAIQHGVPMVGIPFGDQPENMVRVEAKKFGVSIQLKKLKAETL 420

Qy   421 ALKMKQIMEDKRYKSAAVAASVILRSHPLSPTQRLVGWIDHVLQTTGGATHLKPYPVQQPW 480
      |||
Db   421 ALKMKQIMEDKRYKSAAVAASVILRSHPLSPTQRLVGWIDHVLQTTGGATHLKPYPVQQPW 480

Qy   481 HEQYLFQVDFVFLGLTLGLTLWLCLGKLLGMAVWVWLRGARKVKET 523
      |||
Db   481 HEQYLFQVDFVFLGLTLGLTLWLCLGKLLGMAVWVWLRGARKVKET 523

```

RESULT 12

US-10-012-121A-282

; Sequence 282, Application US/10012121A

; Publication No. US20030073810A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.

; APPLICANT: Botstein, David

; APPLICANT: Desnoyers, Luc

; APPLICANT: Eaton, Dan l.

; APPLICANT: Ferrara, Napoleone

; APPLICANT: Fong, Sherman

; APPLICANT: Gao, Wei-Qiang

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Grimaldi, Christopher J.

; APPLICANT: Gurney, Austin L.

; APPLICANT: Hillan, Kenneth J.

; APPLICANT: Pan, James



```
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830P1C20
; CURRENT APPLICATION NUMBER: US/10/012,121A
; CURRENT FILING DATE: 2001-12-07
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 282
; LENGTH: 523
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-012-121A-282
```

```
Query Match          100.0%; Score 2768; DB 14; Length 523;
Best Local Similarity 100.0%; Pred. No. 6.6e-272;
Matches 523; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      1 MAGQRVLLLVGFLLPGVLLSEAAKILTISTVGGSHYLLMDRVSQILQDHGHNVTMLNHR 60
        |||
Db      1 MAGQRVLLLVGFLLPGVLLSEAAKILTISTVGGSHYLLMDRVSQILQDHGHNVTMLNHR 60

Qy     61 GPFMPDFKKEEKSQVISWLPEDHQREFKKSFDFFLEETLGGRGKFENLLNVLEYLALQ 120
        |||
Db     61 GPFMPDFKKEEKSQVISWLPEDHQREFKKSFDFFLEETLGGRGKFENLLNVLEYLALQ 120

Qy    121 CSHFLNRKDIMDSLKNENFDMVIVETFDYCPFLIAEKLKGKPFVAILSTSFGSLEFGLPIP 180
        |||
Db    121 CSHFLNRKDIMDSLKNENFDMVIVETFDYCPFLIAEKLKGKPFVAILSTSFGSLEFGLPIP 180

Qy    181 LSYVPVFRSLLTDHMDFWGRVKNFLMFFSFCRRQOHMQSTFDNTIKEHFTEGSRPVLSHL 240
        |||
Db    181 LSYVPVFRSLLTDHMDFWGRVKNFLMFFSFCRRQOHMQSTFDNTIKEHFTEGSRPVLSHL 240

Qy    241 LLKAELWFINSDFAFDFARPLLNTVYVGGIMEKPIKVPVQDLENFIAKFGDSGFVLVTL 300
        |||
Db    241 LLKAELWFINSDFAFDFARPLLNTVYVGGIMEKPIKVPVQDLENFIAKFGDSGFVLVTL 300

Qy    301 GSMVNTCQNPEIFKEMNNAFAHLPQGVIWKCQCSHWPKDVHLAANVKIVDWLPQSDLLAH 360
        |||
Db    301 GSMVNTCQNPEIFKEMNNAFAHLPQGVIWKCQCSHWPKDVHLAANVKIVDWLPQSDLLAH 360

Qy    361 PSIRLFVTHGGQNSIMEAIQHGVPMVGIPPLFGDQPENMVRVEAKKFGVSIQLKKLKAETL 420
        |||
Db    361 PSIRLFVTHGGQNSIMEAIQHGVPMVGIPPLFGDQPENMVRVEAKKFGVSIQLKKLKAETL 420

Qy    421 ALKMKQIMEDKRYKSAAVAASVILRSHPLSPTQRLVGWIDHVLQTTGGATHLKPYPVQQPW 480
        |||
Db    421 ALKMKQIMEDKRYKSAAVAASVILRSHPLSPTQRLVGWIDHVLQTTGGATHLKPYPVQQPW 480

Qy    481 HEQYLFDFVFVFLGLTLGLTLWLCGKLLGMAVWWLRGARKVKET 523
        |||
Db    481 HEQYLFDFVFVFLGLTLGLTLWLCGKLLGMAVWWLRGARKVKET 523
```

```
RESULT 13
US-10-006-116A-282
```

; Sequence 282, Application US/10006116A  
; Publication No. US20030082626A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan l.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, Christopher J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth J.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; TITLE OF INVENTION: Acids Encoding the Same  
; FILE REFERENCE: P2830P1C15  
; CURRENT APPLICATION NUMBER: US/10/006,116A  
; CURRENT FILING DATE: 2001-12-16  
; PRIOR APPLICATION NUMBER: 60/098716  
; PRIOR FILING DATE: 1998-09-01  
; PRIOR APPLICATION NUMBER: 60/098723  
; PRIOR FILING DATE: 1998-09-01  
; PRIOR APPLICATION NUMBER: 60/098749  
; PRIOR FILING DATE: 1998-09-01  
; PRIOR APPLICATION NUMBER: 60/098750  
; PRIOR FILING DATE: 1998-09-01  
; PRIOR APPLICATION NUMBER: 60/098803  
; PRIOR FILING DATE: 1998-09-02  
; PRIOR APPLICATION NUMBER: 60/098821  
; PRIOR FILING DATE: 1998-09-02  
; PRIOR APPLICATION NUMBER: 60/098843  
; PRIOR FILING DATE: 1998-09-02  
; PRIOR APPLICATION NUMBER: 60/099536  
; PRIOR FILING DATE: 1998-09-09  
; PRIOR APPLICATION NUMBER: 60/099596  
; PRIOR FILING DATE: 1998-09-09  
; PRIOR APPLICATION NUMBER: 60/099598  
; PRIOR FILING DATE: 1998-09-09  
; PRIOR APPLICATION NUMBER: 60/099602  
; PRIOR FILING DATE: 1998-09-09  
; PRIOR APPLICATION NUMBER: 60/099642  
; PRIOR FILING DATE: 1998-09-09  
; PRIOR APPLICATION NUMBER: 60/099741  
; PRIOR FILING DATE: 1998-09-10  
; PRIOR APPLICATION NUMBER: 60/099754  
; PRIOR FILING DATE: 1998-09-10  
; PRIOR APPLICATION NUMBER: 60/099763  
; PRIOR FILING DATE: 1998-09-10  
; PRIOR APPLICATION NUMBER: 60/099792  
; PRIOR FILING DATE: 1998-09-10  
; PRIOR APPLICATION NUMBER: 60/099808  
; PRIOR FILING DATE: 1998-09-10  
; PRIOR APPLICATION NUMBER: 60/099812

; PRIOR FILING DATE: 1998-09-10  
; PRIOR APPLICATION NUMBER: 60/099815  
; PRIOR FILING DATE: 1998-09-10  
; PRIOR APPLICATION NUMBER: 60/099816  
; PRIOR FILING DATE: 1998-09-10  
; PRIOR APPLICATION NUMBER: 60/100385  
; PRIOR FILING DATE: 1998-09-15  
; PRIOR APPLICATION NUMBER: 60/100388  
; PRIOR FILING DATE: 1998-09-15  
; PRIOR APPLICATION NUMBER: 60/100390  
; PRIOR FILING DATE: 1998-09-15  
; PRIOR APPLICATION NUMBER: 60/100584  
; PRIOR FILING DATE: 1998-09-16  
; PRIOR APPLICATION NUMBER: 60/100627  
; PRIOR FILING DATE: 1998-09-16  
; PRIOR APPLICATION NUMBER: 60/100661  
; PRIOR FILING DATE: 1998-09-16  
; PRIOR APPLICATION NUMBER: 60/100662  
; PRIOR FILING DATE: 1998-09-16  
; PRIOR APPLICATION NUMBER: 60/100664  
; PRIOR FILING DATE: 1998-09-16  
; PRIOR APPLICATION NUMBER: 60/100683  
; PRIOR FILING DATE: 1998-09-17  
; PRIOR APPLICATION NUMBER: 60/100684  
; PRIOR FILING DATE: 1998-09-17  
; PRIOR APPLICATION NUMBER: 60/100710  
; PRIOR FILING DATE: 1998-09-17  
; PRIOR APPLICATION NUMBER: 60/100711  
; PRIOR FILING DATE: 1998-09-17  
; PRIOR APPLICATION NUMBER: 60/100848  
; PRIOR FILING DATE: 1998-09-18  
; PRIOR APPLICATION NUMBER: 60/100849  
; PRIOR FILING DATE: 1998-09-18  
; PRIOR APPLICATION NUMBER: 60/100919  
; PRIOR FILING DATE: 1998-09-17  
; PRIOR APPLICATION NUMBER: 60/100930  
; PRIOR FILING DATE: 1998-09-17  
; PRIOR APPLICATION NUMBER: 60/101014  
; PRIOR FILING DATE: 1998-09-18  
; PRIOR APPLICATION NUMBER: 60/101068  
; PRIOR FILING DATE: 1998-09-18  
; PRIOR APPLICATION NUMBER: 60/101071  
; PRIOR FILING DATE: 1998-09-18  
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; PRIOR FILING DATE: 1998-09-22  
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; PRIOR APPLICATION NUMBER: 60/101472  
; PRIOR FILING DATE: 1998-09-23  
; PRIOR APPLICATION NUMBER: 60/101474  
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; PRIOR FILING DATE: 1998-09-23  
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; PRIOR FILING DATE: 1998-09-23  
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; PRIOR FILING DATE: 1998-09-23

; PRIOR APPLICATION NUMBER: 60/101479  
; PRIOR FILING DATE: 1998-09-23  
; PRIOR APPLICATION NUMBER: 60/101738  
; PRIOR FILING DATE: 1998-09-24  
; PRIOR APPLICATION NUMBER: 60/101741  
; PRIOR FILING DATE: 1998-09-24  
; PRIOR APPLICATION NUMBER: 60/101743  
; PRIOR FILING DATE: 1998-09-24  
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; PRIOR FILING DATE: 1998-09-24  
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; PRIOR APPLICATION NUMBER: 60/102484  
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; PRIOR APPLICATION NUMBER: 60/102571  
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; PRIOR APPLICATION NUMBER: 60/102684  
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; PRIOR FILING DATE: 1998-10-01  
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; PRIOR FILING DATE: 1998-10-07  
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; PRIOR APPLICATION NUMBER: 60/103633  
; PRIOR FILING DATE: 1998-10-08  
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; PRIOR APPLICATION NUMBER: 60/103679

; PRIOR FILING DATE: 1998-10-08  
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; PRIOR FILING DATE: 1998-10-08  
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; PRIOR APPLICATION NUMBER: 60/105000  
; PRIOR FILING DATE: 1998-10-20  
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; PRIOR FILING DATE: 1998-10-21  
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; PRIOR FILING DATE: 1998-10-22  
; PRIOR APPLICATION NUMBER: 60/105266  
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; PRIOR APPLICATION NUMBER: 60/105693  
; PRIOR FILING DATE: 1998-10-26  
; PRIOR APPLICATION NUMBER: 60/105694  
; PRIOR FILING DATE: 1998-10-26  
; PRIOR APPLICATION NUMBER: 60/105807  
; PRIOR FILING DATE: 1998-10-27  
; PRIOR APPLICATION NUMBER: 60/105881  
; PRIOR FILING DATE: 1998-10-27  
; PRIOR APPLICATION NUMBER: 60/105882  
; PRIOR FILING DATE: 1998-10-27  
; PRIOR APPLICATION NUMBER: 60/106023  
; PRIOR FILING DATE: 1998-10-28

Query Match 100.0%; Score 2768; DB 14; Length 523;  
Best Local Similarity 100.0%; Pred. No. 6.6e-272;  
Matches 523; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAGQRVLLLVGFLLPGVLLSEAAKILTISTVGGSHYLLMDRVSQILQDHGHNVMTMLNHKR 60  
|  
Db 1 MAGQRVLLLVGFLLPGVLLSEAAKILTISTVGGSHYLLMDRVSQILQDHGHNVMTMLNHKR 60

Qy 61 GPFMPDFKKEEKSQVISWLAPEDHQREFKKSFDFFLEETLGGRGKFENLLNVLEYLALQ 120  
|  
Db 61 GPFMPDFKKEEKSQVISWLAPEDHQREFKKSFDFFLEETLGGRGKFENLLNVLEYLALQ 120

Qy 121 CSHFLNRKDIMDSLKNENFDMVIVETFDYCPFLIAEKLKGPVAILSTSFGSLEFGLPIP 180  
|  
Db 121 CSHFLNRKDIMDSLKNENFDMVIVETFDYCPFLIAEKLKGPVAILSTSFGSLEFGLPIP 180

Qy 181 LSYVPVFRSLLTDHMDFWGRVKNFLMFFSFCRRQQHMQSTFDNTIKEHFTEGSRPVLSHL 240  
|  
Db 181 LSYVPVFRSLLTDHMDFWGRVKNFLMFFSFCRRQQHMQSTFDNTIKEHFTEGSRPVLSHL 240

Qy 241 LLKAELWFINSDFAFDFARPLLNPNTVYVGGLMEKPIKPVQDLENFIAKFGDSGFVLVTL 300  
|  
Db 241 LLKAELWFINSDFAFDFARPLLNPNTVYVGGLMEKPIKPVQDLENFIAKFGDSGFVLVTL 300

Qy 301 GSMVNTCQNPEIFKEMNNAFAHLPQGVIWKCQCSHWPKDVHLAANVKIVDWLPQSDLLAH 360  
|  
Db 301 GSMVNTCQNPEIFKEMNNAFAHLPQGVIWKCQCSHWPKDVHLAANVKIVDWLPQSDLLAH 360

Qy 361 PSIRLFVTHGGQNSIMEAIQHGVPMVGIPFLFGDQPENMVRVEAKKFGVSIQLKKLKAETL 420  
 |||  
 Db 361 PSIRLFVTHGGQNSIMEAIQHGVPMVGIPFLFGDQPENMVRVEAKKFGVSIQLKKLKAETL 420  
 Qy 421 ALKMKQIMEDKRYKSAAVAASVILRSHPLSPTQRLVGWIDHVLQTTGGATHLKPVFQQPW 480  
 |||  
 Db 421 ALKMKQIMEDKRYKSAAVAASVILRSHPLSPTQRLVGWIDHVLQTTGGATHLKPVFQQPW 480  
 Qy 481 HEQYLFDFVFLGLTLGLTLWLCGKLLGMAVWWLRGARKVKET 523  
 |||  
 Db 481 HEQYLFDFVFLGLTLGLTLWLCGKLLGMAVWWLRGARKVKET 523

RESULT 14

US-10-006-117A-282

; Sequence 282, Application US/10006117A

; Publication No. US20030082627A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.

; APPLICANT: Botstein, David

; APPLICANT: Desnoyers, Luc

; APPLICANT: Eaton, Dan l.

; APPLICANT: Ferrara, Napoleone

; APPLICANT: Fong, Sherman

; APPLICANT: Gao, Wei-Qiang

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Grimaldi, Christopher J.

; APPLICANT: Gurney, Austin L.

; APPLICANT: Hillan, Kenneth J.

; APPLICANT: Pan, James

; APPLICANT: Paoni, Nicholas F.

; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

; TITLE OF INVENTION: Acids Encoding the Same

; FILE REFERENCE: P2830P1C13

; CURRENT APPLICATION NUMBER: US/10/006,117A

; CURRENT FILING DATE: 2002-03-19

; Prior Application removed - See File Wrapper or Palm

; PRIOR FILING DATE: 2001-07-09

; NUMBER OF SEQ ID NOS: 477

; SEQ ID NO 282

; LENGTH: 523

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-006-117A-282

Query Match 100.0%; Score 2768; DB 14; Length 523;

Best Local Similarity 100.0%; Pred. No. 6.6e-272;

Matches 523; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAGQRVLLLVGFLLPGVLLSEAAKILTISTVGGSHYLLMDRVSQILQDHGHNVTMLNHKR 60  
 |||  
 Db 1 MAGQRVLLLVGFLLPGVLLSEAAKILTISTVGGSHYLLMDRVSQILQDHGHNVTMLNHKR 60  
 Qy 61 GPFMPDFKKEEKSYQVISWLAPEDHQREFKKSFDFFLEETLGGRGKFENLLNVLEYLALQ 120  
 |||

Db 61 GPFMPDFKKEEKSYQVISWLPEDHQREFKKSFDFFLEETLGGRGKFENLLNVLEYLALQ 120  
 Qy 121 CSHFLNRKDIMDSLKNENFDMVIVETFDYCPFLIAEKLGPVAILSTSFGSLEFGLPIP 180  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 121 CSHFLNRKDIMDSLKNENFDMVIVETFDYCPFLIAEKLGPVAILSTSFGSLEFGLPIP 180  
 Qy 181 LSYVPVFRSLTLDHMDFWGRVKNFLMFFSFCRRQQHMQSTFDNTIKEHFTEGSRPVLSHL 240  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 181 LSYVPVFRSLTLDHMDFWGRVKNFLMFFSFCRRQQHMQSTFDNTIKEHFTEGSRPVLSHL 240  
 Qy 241 LLKAEWLFINSDFAFDFARPLLNTVYVGGLMEKPIKVPQDLENFIAKFGDSGFVLVTL 300  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 241 LLKAEWLFINSDFAFDFARPLLNTVYVGGLMEKPIKVPQDLENFIAKFGDSGFVLVTL 300  
 Qy 301 GSMVNTCQNPEIFKEMNNAFAHLPQGVWKQCQSHWPKDVHLAANVKIVDWLPQSDLLAH 360  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 301 GSMVNTCQNPEIFKEMNNAFAHLPQGVWKQCQSHWPKDVHLAANVKIVDWLPQSDLLAH 360  
 Qy 361 PSIRLFVTHGGQNSIMEAIQHGVPMVGIPFLFGDQPENMVRVEAKKFGVSIQLKKLKAETL 420  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 361 PSIRLFVTHGGQNSIMEAIQHGVPMVGIPFLFGDQPENMVRVEAKKFGVSIQLKKLKAETL 420  
 Qy 421 ALKMKQIMEDKRYKSAAVAASVILRSHPLSPTQRLVGWIDHVLQTGGATHLKPYPVQQPW 480  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 421 ALKMKQIMEDKRYKSAAVAASVILRSHPLSPTQRLVGWIDHVLQTGGATHLKPYPVQQPW 480  
 Qy 481 HEQYLFDFVFLGLTLGLTLWLCGKLLGMAVWWLRGARKVKET 523  
 ||||||||||||||||||||||||||||||||||||||||||||  
 Db 481 HEQYLFDFVFLGLTLGLTLWLCGKLLGMAVWWLRGARKVKET 523

RESULT 15

US-10-017-527A-282

; Sequence 282, Application US/10017527A

; Publication No. US20030082628A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.

; APPLICANT: Botstein, David

; APPLICANT: Desnoyers, Luc

; APPLICANT: Eaton, Dan I.

; APPLICANT: Ferrara, Napoleone

; APPLICANT: Fong, Sherman

; APPLICANT: Gao, Wei-Qiang

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Grimaldi, Christopher J.

; APPLICANT: Gurney, Austin L.

; APPLICANT: Hillan, Kenneth J.

; APPLICANT: Pan, James

; APPLICANT: Paoni, Nicholas F.

; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

; TITLE OF INVENTION: Acids Encoding the Same

; FILE REFERENCE: P2830P1C63

; CURRENT APPLICATION NUMBER: US/10/017,527A

; CURRENT FILING DATE: 2001-12-13

; PRIOR APPLICATION NUMBER: 60/098716

; PRIOR FILING DATE: 1998-09-01

; PRIOR APPLICATION NUMBER: 60/098723  
; PRIOR FILING DATE: 1998-09-01  
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; PRIOR FILING DATE: 1998-09-01  
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; PRIOR FILING DATE: 1998-09-02  
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; PRIOR FILING DATE: 1998-09-02  
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; PRIOR APPLICATION NUMBER: 60/100385  
; PRIOR FILING DATE: 1998-09-15  
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; PRIOR APPLICATION NUMBER: 60/100684



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; PRIOR FILING DATE: 1998-09-30

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; PRIOR APPLICATION NUMBER: 60/105693  
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; PRIOR APPLICATION NUMBER: 60/105694  
; PRIOR FILING DATE: 1998-10-26  
; PRIOR APPLICATION NUMBER: 60/105807  
; PRIOR FILING DATE: 1998-10-27  
; PRIOR APPLICATION NUMBER: 60/105881

; PRIOR FILING DATE: 1998-10-27  
; PRIOR APPLICATION NUMBER: 60/105882  
; PRIOR FILING DATE: 1998-10-27  
; PRIOR APPLICATION NUMBER: 60/106023  
; PRIOR FILING DATE: 1998-10-28

Query Match 100.0%; Score 2768; DB 14; Length 523;  
Best Local Similarity 100.0%; Pred. No. 6.6e-272;  
Matches 523; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 MAGQRVLLLVGFLPGVLLSEAAKILTISTVGGSHYLLMDRVSQILQDHGHNVMTLNHKR 60
      |||
Db      1 MAGQRVLLLVGFLPGVLLSEAAKILTISTVGGSHYLLMDRVSQILQDHGHNVMTLNHKR 60

Qy     61 GPFMPDFKKEEKSQVISWLAPEDHQREFKKSFDFFLEETLGGRGKFENLLNVLEYLALQ 120
      |||
Db     61 GPFMPDFKKEEKSQVISWLAPEDHQREFKKSFDFFLEETLGGRGKFENLLNVLEYLALQ 120

Qy    121 CSHFLNRKDIMDSLKNENFDMVIVETFDYCPFLIAEKLKGKPFVAILSTSFSGSLEFGLPIP 180
      |||
Db    121 CSHFLNRKDIMDSLKNENFDMVIVETFDYCPFLIAEKLKGKPFVAILSTSFSGSLEFGLPIP 180

Qy    181 LSYVPVERSLLTDHMDFWGRVKNFLMFFSFCRRQQHMQSTFDNTIKEHFTEGSRPVLSHL 240
      |||
Db    181 LSYVPVFRSLLTDHMDFWGRVKNFLMFFSFCRRQQHMQSTFDNTIKEHFTEGSRPVLSHL 240

Qy    241 LLKAELWFINSDFAFDFARPLLNTVYVGGLMKPKPKVPQDLENFIAKFGDSGFVLVTL 300
      |||
Db    241 LLKAELWFINSDFAFDFARPLLNTVYVGGLMKPKPKVPQDLENFIAKFGDSGFVLVTL 300

Qy    301 GSMVNTCQNPEIFKEMNNAFAHLPQGVWKQCQSHWPKDVHLAANVKIVDWLPQSDLLAH 360
      |||
Db    301 GSMVNTCQNPEIFKEMNNAFAHLPQGVWKQCQSHWPKDVHLAANVKIVDWLPQSDLLAH 360

Qy    361 PSIRLFVTHGGQNSIMEAIQHGVPMVGIPFLFGDQPENMVRVEAKKFGVSIQLKKLKAETL 420
      |||
Db    361 PSIRLFVTHGGQNSIMEAIQHGVPMVGIPFLFGDQPENMVRVEAKKFGVSIQLKKLKAETL 420

Qy    421 ALKMKQIMEDKRYKSAAVAASVILRSHPLSPTQRLVGWIDHVLQTGGATHLKPYPVFQQPW 480
      |||
Db    421 ALKMKQIMEDKRYKSAAVAASVILRSHPLSPTQRLVGWIDHVLQTGGATHLKPYPVFQQPW 480

Qy    481 HEQYLFDFVFVLLGLTLGTLWLWLCGKLLGMAVWWLRGARKVKET 523
      |||
Db    481 HEQYLFDFVFVLLGLTLGTLWLWLCGKLLGMAVWWLRGARKVKET 523
```

Search completed: May 7, 2004, 17:34:58  
Job time : 50 secs

OM protein - protein search, using sw model

Run on: May 7, 2004, 17:28:39 ; Search time 45 Seconds  
(without alignments)  
3667.023 Million cell updates/sec

Title: US-10-017-867A-282  
Perfect score: 2768  
Sequence: 1 MAGQRVLLLVGFLLPGVLLS.....GKLLGMAVWVLLRGARKVKET 523

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SPTREMBL\_25:\*

- 1: sp\_archaea:\*
- 2: sp\_bacteria:\*
- 3: sp\_fungi:\*
- 4: sp\_human:\*
- 5: sp\_invertebrate:\*
- 6: sp\_mammal:\*
- 7: sp\_mhc:\*
- 8: sp\_organelle:\*
- 9: sp\_phage:\*
- 10: sp\_plant:\*
- 11: sp\_rodent:\*
- 12: sp\_virus:\*
- 13: sp\_vertebrate:\*
- 14: sp\_unclassified:\*
- 15: sp\_rvirus:\*
- 16: sp\_bacteriap:\*
- 17: sp\_archeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result	%	Query				
No.	Score	Match Length	DB	ID		Description
-----						

1	2754	99.5	523	4	Q8NBP2	Q8nbp2 homo sapien
2	2193	79.2	523	4	Q96DM6	Q96dm6 homo sapien
3	1815	65.6	523	11	Q8R0Y5	Q8r0y5 mus musculu
4	1804	65.2	523	11	Q8JZZ0	Q8jzz0 mus musculu
5	1802	65.1	523	11	Q8VC11	Q8vc11 mus musculu
6	963	34.8	221	4	Q8NAW4	Q8naw4 homo sapien
7	914.5	33.0	252	4	Q8IYS9	Q8iys9 homo sapien
8	792	28.6	302	11	Q8BRY7	Q8bry7 mus musculu
9	727	26.3	541	13	Q98TB5	Q98tb5 gallus gall
10	698	25.2	541	11	Q91W57	Q91w57 mus musculu
11	689.5	24.9	529	6	Q9TSL6	Q9tsl6 macaca fasc
12	685.5	24.8	529	6	O97951	O97951 macaca fasc
13	685.5	24.8	534	11	Q8BWQ1	Q8bwq1 mus musculu
14	684.5	24.7	498	6	Q9BDZ8	Q9bdz8 bos taurus
15	681	24.6	530	11	Q9R110	Q9r110 cavia porce
16	680.5	24.6	534	11	Q9D811	Q9d811 mus musculu
17	680	24.6	529	6	Q9GLD9	Q9gld9 macaca mula
18	677.5	24.5	534	11	Q8R129	Q8r129 mus musculu
19	674.5	24.4	530	11	Q7TT85	Q7tt85 rattus norv
20	673.5	24.3	533	6	O46548	O46548 felis silve
21	672.5	24.3	449	4	Q9H6S4	Q9h6s4 homo sapien
22	670.5	24.2	528	11	Q80X89	Q80x89 mus musculu
23	670	24.2	527	11	Q9ESE4	Q9ese4 mus musculu
24	668	24.1	529	11	Q8R084	Q8r084 mus musculu
25	667.5	24.1	529	11	Q8VIF8	Q8vif8 cavia porce
26	667	24.1	533	6	O46549	O46549 felis silve
27	666.5	24.1	528	6	Q8WN97	Q8wn97 macaca fasc
28	665.5	24.0	533	6	O46423	O46423 felis silve
29	665	24.0	533	6	Q9TSL7	Q9tsl7 macaca fasc
30	664	24.0	531	11	Q8VD45	Q8vd45 rattus norv
31	662	23.9	533	6	Q95KM4	Q95km4 macaca mula
32	661	23.9	528	11	Q8VIF9	Q8vif9 cavia porce
33	660.5	23.9	529	6	Q9GLE0	Q9gle0 macaca mula
34	658	23.8	533	6	Q9BDG7	Q9bdg7 macaca mula
35	650.5	23.5	532	11	Q8K154	Q8k154 mus musculu
36	643	23.2	529	11	Q8BJL9	Q8bjl9 mus musculu
37	637.5	23.0	530	11	Q91WH2	Q91wh2 mus musculu
38	637.5	23.0	532	4	Q8WUQ4	Q8wuq4 homo sapien
39	635.5	23.0	529	6	O18736	O18736 bos taurus
40	635.5	23.0	530	11	Q8K169	Q8k169 mus musculu
41	634	22.9	530	11	Q8VCN3	Q8vcn3 mus musculu
42	627	22.7	530	6	Q9TSM0	Q9tsm0 macaca fasc
43	624.5	22.6	532	6	Q9TSL9	Q9tsl9 macaca fasc
44	621.5	22.5	498	11	Q8VCQ9	Q8vcq9 mus musculu
45	621	22.4	530	6	Q9TSL8	Q9tsl8 macaca fasc

#### ALIGNMENTS

##### RESULT 1

Q8NBP2

ID Q8NBP2 PRELIMINARY; PRT; 523 AA.

AC Q8NBP2;

DT 01-OCT-2002 (TrEMBLrel. 22, Created)

DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)

DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)

DE Hypothetical protein NT2RP2002934.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Ota T., Nishikawa T., Suzuki Y., Kawai-Hio Y., Hayashi K., Ishii S.,  
RA Saito K., Yamamoto J., Wakamatsu A., Nagai T., Nakamura Y.,  
RA Nagahari K., Sugano S., Isogai T.;  
RT "HRI human cDNA sequencing project.";  
RL Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.  
DR EMBL; AK075383; BAC11583.1; -.  
DR GO; GO:0016758; F:transferase activity, transferring hexosyl . . .; IEA.  
DR GO; GO:0008152; P:metabolism; IEA.  
DR InterPro; IPR002213; UDP\_gluco\_trans.  
DR Pfam; PF00201; UDPGT; 1.  
DR PROSITE; PS00375; UDPGT; 1.  
KW Hypothetical protein.  
SQ SEQUENCE 523 AA; 59618 MW; 89928A26AB9C09F5 CRC64;

Query Match 99.5%; Score 2754; DB 4; Length 523;  
Best Local Similarity 99.6%; Pred. No. 8.1e-222;  
Matches 521; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy	1	MAGQRVLLLVGFLPGVLLSEAAKILTISTVGGSHYLLMDRVSQILQDHGHNVMTLNHKR	60
Db	1	MAGQRVLLLVGFLPGVLLSEAAKILTISTVGGSHYLLMDRVSQILQDHGHNVMTLNHKR	60
Qy	61	GPFPMPDFKKEEKSYQVISWLAPEDHQREFKKSFDFFLEETLGGRGKFENLLNVLEYLALQ	120
Db	61	GPFPMPDFKKEEKSYQVISWLAPEDHQREFKKSFDFFLEETLGGRGKFENLLNVLEYLALQ	120
Qy	121	CSHFLNRKDIMDSLKNENFDMVIVETFDCPFLIAEKLKGKPFVAILSTSFSGSLEFGLPIP	180
Db	121	CSHFLNRKDIMDSLKNENFDMVIVETFDCPFLIAEKLKGKPFVAILSTSFSGSLEFGLPIP	180
Qy	181	LSYVPVFRSLLTDHMDFWGRVKNFLMFFSFCRRQQHMQSTFDNTIKEHFTEGSRPVLSHL	240
Db	181	LSYVPVFRSLLTDHMDFWGRVKNFLMFFSFCRRQQHMQSTFDNTIKEHFTEGSRPVLSHL	240
Qy	241	LLKAELWFINSDFAFDFARPLLNTVYVGGLMEKPIKPVPODLENFIAKFGDSGFVLVTL	300
Db	241	LLKAELWFINSDFAFDFARPLLNTVYVGGLMEKPIKPVPODLENFIAKFEDSGFVLVTL	300
Qy	301	GSMVNTCQNPEIFKEMNNAFAHLPQGVWKCQCShWPKDVHLAANVKIVDWLPQSDLLAH	360
Db	301	GSMVNTCQNPEIFKEMNNAFAHLPQGVWKCQCShWPKDVHLAANVKIVDWLPQSDLLAH	360
Qy	361	PSIRLFVTHGGQNSIMEAIQHGVPVVGIPLEFGDQPENMVRVEAKKFGVSIQLKKLKAETL	420
Db	361	PSIRLFVTHGGQNSIMEAIQHGVPVVGIPLEFGDQPENMVRVEAKKFGVSIQLKKLKAETL	420
Qy	421	ALKMKQIMEDKRYKSAVAASVILRSHPLSPTQRLVGWIDHVLQTTGGATHLKPYVFQQPW	480
Db	421	ALKMKQIMEDKRYKSAVAASVILRSHPLSPTQRLVGWIDHVLQTTGGATHLKPYVFQQPW	480

QY 481 HEQYLFDFVFVFLGLTLGLTLWLWLCGKLLGMAVWWLRGARKVKET 523  
||||| |||||||||||||||||||||||||||||||||||  
Db 481 HEQYLLDVVFVFLGLTLGLTLWLWLCGKLLGMAVWWLRGARKVKET 523

RESULT 2

Q96DM6

ID Q96DM6 PRELIMINARY; PRT; 523 AA.  
AC Q96DM6;  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Hypothetical protein FLJ32504.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Small intestine;  
RA Kawakami B., Sugiyama A., Takemoto M., Sugiyama T., Irie R.,  
RA Otsuki T., Sato H., Wakamatsu A., Ishii S., Yamamoto J., Isono Y.,  
RA Kawai-Hio Y., Saito K., Nishikawa T., Kimura K., Yamashita H.,  
RA Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K., Wagatsuma M.,  
RA Murakawa K., Kanehori K., Takahashi-Fujii A., Oshima A., Suzuki Y.,  
RA Sugano S., Nagahari K., Masuho Y., Nagai K., Isogai T.;  
RT "NEDO human cDNA sequencing project.";  
RL Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.  
DR EMBL; AK057066; BAB71358.1; -.  
DR GO; GO:0016758; F:transferase activity, transferring hexosyl . . .; IEA.  
DR GO; GO:0008152; P:metabolism; IEA.  
DR InterPro; IPR002213; UDP\_gluco\_trans.  
DR Pfam; PF00201; UDPGT; 1.  
DR PROSITE; PS00375; UDPGT; 1.  
KW Hypothetical protein.  
SQ SEQUENCE 523 AA; 59148 MW; 2034D6E90863EA8E CRC64;

Query Match 79.2%; Score 2193; DB 4; Length 523;  
Best Local Similarity 78.8%; Pred. No. 7.5e-175;  
Matches 413; Conservative 45; Mismatches 64; Indels 2; Gaps 2;

Qy 1 MAGQRVLLLVGFLLPGVLLSEAAKILTISTVGGSHYLLMDRVSQILQDHGHNVTMLNHKR 60  
| ||||| || ||||||||||||||||:|||||:|||||:||||| |:  
Db 1 MVGQRVLLLVAFLLSGVLLSEAAKILTISTLGGSHYLLLD RVSQILQE HGHNV TML-HQS 59  
  
Qy 61 GPFM-PDFKKEEKSYQVISWLAPEDHQREFKKSFDFFLEETLGGRGKFENLLNVLEYLAL 119  
| |: || |:||||||| |:||||: || || :| || : | |: :|  
Db 60 GKFLIPDIKEEEKSYQVIRWFSPEDHQKRIKKHFD SYIETALDGRKESEALVKLMEIFGT 119  
  
Qy 120 QCSHFLNRKDIMDSLKNENFDMVIVETFDYCPFLIAEKL GKPFVAILSTSFGLPI 179  
|||: |:||||||| |:| || ||:| ||||| ||||| |:||||:|  
Db 120 QCSYLLSRKDIMDSLKNENCDLVFEAFDFCSFLIAEKL VKPFVAILPTTFGLPS 179  
  
Qy 180 PLSYVPVFRSLLTDHMDFWGRVKNFLMFFSF CRRQQHMQSTFDNTIKEHFT EGSRPVLSH 239  
||||||| ||||||||||||||||||| | | ||||||||| |||||||  
Db 180 PLSYVPVFRSLLTDHMDFWGRVKNFLMFFSF SRSQWDMQSTFDNTIKEHFP EGSRPVLSH 239

Qy 240 LLLKAELWFINSDFAFDFARPLLNTVYVGGLMEKPIKVPQDLENFIAKFGDSGFVLVT 299  
 |||||:|||||:|||||:|||||  
 Db 240 LLLKAELWVFNSDFAFDFARPLLNTVYIGGLMEKPIKVPQDLNFIANFGDAGFVLVA 299

Qy 300 LGSMVNTCQNPEIFKEMNNAFAHLPQGVIWKCQCSHWPKDVHLAANVKIVDWLPQSDLLA 359  
 |||:| |: |: |:|:||||| || |||:||||| |||||  
 Db 300 FGSMLNTHQSQEVLKKMHNAFAHLPQGVIWTCQSSHWPRDVHLATNVKIVDWLPQSDLLA 359

Qy 360 HPSIRLFVTHGGQNSIMEAIQHGVPMVGIPLFGDQPENMVRVEAKKFGVSIQLKKLKAET 419  
 |||||:| |:|:|||||:| || ||| ||:||||:| ::|:  
 Db 360 HPSIRLFVTHGGQNSVMETIRHGVPMVGLPVNGDQHGNMVRVAKNYGVSIRLNQVTADT 419

Qy 420 LALKMKQIMEDKRYKSAAVAASVILRSHPLSPTQRLVGWIDHVLQTTGGATHLKPYVFQQP 479  
 | | |||:||||| ||||| | ||| |||||:|||||  
 Db 420 LTLTMKQVIEDKRYKSAVAASVILHSQPLSPAQRLVGWIDHILQTTGGATHLKPYVFQQP 479

Qy 480 WHEQYLFDFVFLGLTLGLTLWLCGKLLGMAVWWLRGARKVKET 523  
 ||||| |||||:|||||: |||||:  
 Db 480 WHEQYLIDVFLGLTLGLTMWLCGKLLGVVARWLRGARKVKKT 523

# RESULT 3

Q8ROY5

ID Q8ROY5 PRELIMINARY; PRT; 523 AA.  
 AC Q8ROY5;  
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)  
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Hypothetical protein.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Liver;  
 RA Strausberg R.;  
 RL Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.  
 DR EMBL; BC025940; AAH25940.1; -.  
 DR GO; GO:0016758; F:transferase activity, transferring hexosyl . . .; IEA.  
 DR GO; GO:0008152; P:metabolism; IEA.  
 DR InterPro; IPR002213; UDP\_gluco\_trans.  
 DR Pfam; PF00201; UDPGT; 1.  
 DR PROSITE; PS00375; UDPGT; 1.  
 KW Hypothetical protein.  
 SQ SEQUENCE 523 AA; 59742 MW; F2EF34F41C3DEB95 CRC64;

Query Match 65.6%; Score 1815; DB 11; Length 523;  
 Best Local Similarity 65.4%; Pred. No. 3.3e-143;  
 Matches 342; Conservative 73; Mismatches 106; Indels 2; Gaps 2;

Qy 1 MAGQRVLLLVGFLLPGVLLSEAAKILTISTVGGSHYLLMDRVSQILQDHGHNVTMLNHRK 60  
 || | ||| | | ||| |||||: |||:|:||||| ||:| | ::  
 Db 1 MAAHRSWLLVSFFLLLEVLLLEAAKILTISTLSASHYILMNRVSQILQGGGHDVIKLLYEG 60

Qy 61 GPFMPDFKKEEKSYQVISWLAPEDHQREFKKSFDFFLEETLGGRGKFENLLNVLEYLALQ 120  
 | :|||:| ||||:| ||| |: |: : :| || |: || : :| |



Db 61 GD-IPDFRKENSSYQVINWRLPEDQQKTFENRWHRLIDEYAYGRSKYHTLLKIHQYFADL 119

Qy 121 CSHFLNRKDIMDSLKNENFDMVIVETFDYCPFLIAEKLKGKPFVAILSTSFGLSLEFGLP-I 179  
 ||| |:||||: |: ||||:|::: | | ||| |||| | |: | | ::|||

Db 120 CSHLLSRKDIMELLQKENFDLVLLDSMDLCSFLIVEKLGKRFVSFLPFQFSYMDFGLPNA 179

Qy 180 PLSYVPVFRSLTLDHMDFWGRVKNFLMFFSFCCRQQHMQSTFDNTIKEHFTEGSRPVLSH 239  
 |||| |: | ||| ||||| |||| | ::: : | : ||:| | ||:| |

Db 180 PLSYAPVYGSLTDQMDFWGRVKNILMFFHFTKKRRDIFSQYGNTVQEHFAEGSQPVLS 239

Qy 240 LLLKAELWFINSDFAFDFARPLLPNTVYVGGLMKPKPKVPQDLENFIAKFGDSGFVLVT 299  
 ||||| |:| | |||| | ||||| :|:|:|:|:|:|:|:|:|:|:|:|

Db 240 LLLKAELWFVNSDFALDFARPLFPNTVYVGGLLDKPVQPIPDLEDFISQFGDSGFVLVA 299

Qy 300 LGSMVNTCQNPEIFKEMNNAFAHLPQGVIWKCQCSEHWPCKDVHLAANVKIVDWLPQSDLLA 359  
 | |:|: |: || ||||:| ||||| |: | |||| | | |||:| | | |||

Db 300 LDSVSMIQSKEIIKEMNSAFAHLPQGVLTCKSSHWPCKDVSLAPNVKIMDWLPQIDLLA 359

Qy 360 HPSIRLFVTHGGQNSIMEAIQHGVPMVGIPFGDQPENMVRVEAKKFGVSIQLKKLKAET 419  
 ||||| |||| | |:| |: |||| | ||||| ||||| |||||: ||||:

Db 360 HPSIRLFVTHGGMNSVMEAVHHGVPMVGIPFFGDQPENMVRVEAKNLGVSIQLQTLKAES 419

Qy 420 LALKMKQIMEDKRYKSAAVAASVILRSHPLSPTQRLVGWIDHVLQTGGATHLKPYPVQQP 479  
 | ||::|:|:|:|:|:|: | | ||||:| ||||| |:| |||| | |||

Db 420 FLLTMKEVIEDQRYKTAAMASKVIRNSHPLTPAQLVGWIDHILQTGGAHLKPYAFQQP 479

Qy 480 WHEQYLFDFVFLGLTLGLTLWLCLGKLLGMAVWWLRGARKVKE 522  
 ||||: ||:| ||||| |||| | |: | :| :|||:

Db 480 WHEQYMLDVFLGLTLGLTLWLSVKVLVAVTRYLSISRKVKQ 522

# RESULT 4

Q8JZZ0

ID Q8JZZ0 PRELIMINARY; PRT; 523 AA.

AC Q8JZZ0;

DT 01-OCT-2002 (TrEMBLrel. 22, Created)

DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

DE Hypothetical protein MGC37820.

GN AI313915.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI\_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Liver;

RA Strausberg R.;

RL Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.

DR EMBL; BC034837; AAH34837.1; -.

DR MGD; MGI:2145969; AI313915.

DR GO; GO:0016758; F:transferase activity, transferring hexosyl . . .; IEA.

DR GO; GO:0008152; P:metabolism; IEA.

DR InterPro; IPR002213; UDP\_gluco\_trans.

DR Pfam; PF00201; UDPGT; 1.

DR PROSITE; PS00375; UDPGT; 1.

KW Hypothetical protein.

SQ SEQUENCE 523 AA; 59662 MW; 4F7BD5ACBAFB5127 CRC64;

Query Match 65.2%; Score 1804; DB 11; Length 523;  
Best Local Similarity 65.4%; Pred. No. 2.7e-142;  
Matches 342; Conservative 69; Mismatches 110; Indels 2; Gaps 2;

```
Qy      1 MAGQRVLLLVGFLLPGVLLSEAAKILTISTVGGSHYLLMDRVSQILQDHGHNVMTLNHKR 60
      || | ||: || |:| ||||| ||||: |||::: ||||:| : |||| | ::
Db      1 MAAHRRWLLMSFLFLEVILLEAAKILTISTLSASHYIVISRVSQVLHEGGHNVTKLLYES 60

Qy     61 GPFMPDFKKEEKSYQVISWLAPEDHQREFKKSFDFFLEETLGGRGKFENLLNVLEYLALQ 120
      :||:|:|: ||||:| ||| :::| || || | || : :|
Db     61 AN-IPDFRKEKPSYQVINWRPPEDQEKKFADLRHRLTEEITYGRSKHHTLLKIHQYFGDL 119

Qy    121 CSHFLNRKDIMDSLKNENFDMVIVETFDYCPFLIAEKLKGKPFVAILSTSFSGSLEFGLP-I 179
      || |:||||| |||||:|:|:| | || ||||| ||: | | :|||
Db    120 CSQLLSRKDIMDFLKNENFDVLVLDSDMLCSLLIVEKLGKRFVSFLPFQFSYMDFGLPISA 179

Qy    180 PLSYVPVFRSLLTDHMDFWGRVKNFLMFFSFCCRQOHMQSTFDNTIKEHFTEGSRPVLSH 239
      |||| ||: | ||| ||||| ||||| | :|: : | :|:|:| ||| :|||
Db    180 PLSYAPVYGSLTDQMDFWGRVKNFLMFLDFSMKQREILSQYDSTIQEHFVEGSQPVLS 239

Qy    240 LLLKAELWFINSDFAFDFARPLLPNTVYVGGLMEKPIKVPQDLENFIAKEFGDSGFVLVT 299
      ||||| ||||: ||||| ||||| ||||| ||||: ||||: ||||: ||||: |||||
Db    240 LLLKAELWFVNSDFALDFARPLFPNTVYVGGLLDKPVQPIQDLENFISQFGDSGFVLVA 299

Qy    300 LGSMVNTCQNPEIFKEMNNAFAHLPQGVIWKQCQSHWPKDVHLAANVKIVDWLPQSDLLA 359
      |||:|: |: || ||||: ||||| ||||: | |: ||||| ||: ||||: ||||: ||||
Db    300 LGSIVSMIQSKEIIKEMNSAFAHLPQGVLTCTKTSWPKDVSLASNVKIMDWLPQTDLA 359

Qy    360 HPSIRLFVTHGGQNSIMEAIQHGVPMVGIPLEFGDQPENMVRVEAKKFGVSIQLKKLKAET 419
      ||||| ||||| ||: |||: ||||| ||||| ||||| ||||| ||||| ||||: ||||:
Db    360 HPSIRLFVTHGGMNSVMEAVHHGVPMVGIPFFFDQPENMVRVEAKNLGVSIQLQTLKAES 419

Qy    420 LALKMKQIMEDKRYKSAAVAASVILRSHPLSPTQRLVGWIDHVLQTTGATHLKPYPVFQQP 479
      || ||:|: ||||| ||||:|: | ||||:| |||: ||||: ||||| ||||| ||||
Db    420 FALTMKKIIEDKRYKSAAMASKIIRHSHPLTPAQRLVGWIDHILQTTGAAHLKPYAFQQP 479

Qy    480 WHEQYLFDFVFLGLTLGLTLWLCLGKLLGMAVWWLRGARKVKE 522
      ||||: |||: |||| ||||| |:| :| | ||||
Db    480 WHEQYMLDVFLFLGLMLGLTLWLSVKVLVAVTRYLSIATKVKE 522
```

#### RESULT 5

Q8VC11

ID Q8VC11 PRELIMINARY; PRT; 523 AA.

AC Q8VC11;

DT 01-MAR-2002 (TrEMBLrel. 20, Created)

DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

DE Hypothetical protein (Hypothetical UDP-glucoronosyl and UDP-glucosyl  
transferase containing protein).

GN AI313915.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI\_TaxID=10090;

RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Liver;  
 RA Strausberg R.;  
 RL Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=Liver;  
 RX MEDLINE=22354683; PubMed=12466851;  
 RA The FANTOM Consortium,  
 RA the RIKEN Genome Exploration Research Group Phase I & II Team;  
 RT "Analysis of the mouse transcriptome based on functional annotation of  
 RT 60,770 full-length cDNAs.";  
 RL Nature 420:563-573(2002).  
 DR EMBL; BC022134; AAH22134.1; -.  
 DR EMBL; AK050128; BAC34080.1; -.  
 DR MGD; MGI:2145969; AI313915.  
 DR GO; GO:0016758; F:transferase activity, transferring hexosyl . . .; IEA.  
 DR GO; GO:0008152; P:metabolism; IEA.  
 DR InterPro; IPR002213; UDP\_gluco\_trans.  
 DR Pfam; PF00201; UDPGT; 1.  
 DR PROSITE; PS00375; UDPGT; 1.  
 KW Hypothetical protein.  
 SQ SEQUENCE 523 AA; 59672 MW; BC7BD6ADF197ADD9 CRC64;

Query Match 65.1%; Score 1802; DB 11; Length 523;  
 Best Local Similarity 65.4%; Pred. No. 4e-142;  
 Matches 342; Conservative 68; Mismatches 111; Indels 2; Gaps 2;

Qy	1	MAGQRVLLLVGFLLPGVLLSEAAKILTISTVGGSHYLLMDRVSQILQDHGHNVMTLNHKR	60
		:     :           :    :  :        :	
Db	1	MAAHRRWLLMSFLFLEVILLEAAKILTISTLSASHYIVISRVSQVLHEGGHNVTKLLYES	60
Qy	61	GPFPDFKKEEKSYQVISWLAPEDHQREFKKSFDFFLEETLGGRGKFENLLNVLEYLALQ	120
		:   : :     :      :               : :	
Db	61	AN-IPDFRKEKPSYQVINWRPPEDQEKKFADLRHRLTEEITYGRSKHHTLLKIHQYFGDL	119
Qy	121	CSHFLNRKDIMDSLKNENFDMVIVETFDYCPFLIAEKLKGKPFVAILSTSFGSLEFGLP-I	179
		:           : : :                :     :	
Db	120	CSQLSRKDIMDFLKNENFDLVLDSMDLCSLLIVEKLGKRFVSFLPFQFSYMDFGFLPSA	179
Qy	180	PLSYVPVFRSLTLDHMDFWGRVKNFLMFFSFCRRQQHMQSTFDNTIKEHFTEGSRPVLSH	239
		:                     : :   : : :      :	
Db	180	PLSYAPVYGSLTDQMDFWGRVKNFLMFLDFSMKQREILSQYDSTIQEHFVEGSQPVLS	239
Qy	240	LLLKAELWFINSDFAFDFARPLLNTVYVGGLMKPKVPQDLENFIAKFGDSGFVLVT	299
		:                  : : : :       :	
Db	240	LLLKAELWFVNSDFALDFARPLFPNTVYVGGLLDKPVQPIPDLENFISQFGDSGFVLVA	299
Qy	300	LGSVMNTCQNPEIFKEMNNAFAHLPQGVWIKQCQSHWPKDVHLAANVKIVDWLPQSDLLA	359
		: :  :        :       :   :              :    :	
Db	300	LGSIVSMIQSKEIIKEMNSAFAHLPQGVLTCTSHWPKDVSLAPNVKIMDWLPQTDLLA	359
Qy	360	HPSIRLFVTHGGQNSIMEAIQHGVPVMGIPFQDQPENMVRVEAKKFGVSIQLKKLKAET	419
		: :                     :     :	
Db	360	HPSIRLFVTHGGMNSVMEAVHHGVPVMGIPFFFDQPENMVRVEAKNLGVSIQLQTLKAES	419

Qy 420 LALKMKQIMEDKRYKSAAVAASVILRSHPLSPTQRLVGWIDHVLQTGGATHLKPYVFQQP 479  
 || ||:|:|||||||:|: | ||||:| |||:||||:||||| |||| ||||  
 Db 420 FALTMKKIIEDKRYKSAAMASKIIRHSHPLTPAQRLLGWIDHILQTGGAAHLKPYAFQQP 479  
 Qy 480 WHEQYLFDFVFLGLTLGLTLWLCLCGKLLGMAVWWLRGARKVKE 522  
 ||||: |||:|||| | |||| | |: | :| | ||||  
 Db 480 WHEQYMLDVFLFLLGLMLGLTLWLSVKVLVAVTRYLSIATKVKE 522

RESULT 6

Q8NAW4

ID Q8NAW4 PRELIMINARY; PRT; 221 AA.  
 AC Q8NAW4;  
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE Hypothetical protein FLJ34658.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Kidney;  
 RA Tashiro H., Yamazaki M., Watanabe K., Kumagai A., Itakura S.,  
 RA Fukuzumi Y., Fujimori Y., Komiyama M., Sugiyama T., Irie R.,  
 RA Otsuki T., Sato H., Wakamatsu A., Ishii S., Yamamoto J., Isono Y.,  
 RA Kawai-Hio Y., Saito K., Nishikawa T., Kimura K., Yamashita H.,  
 RA Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K., Wagatsuma M.,  
 RA Murakawa K., Kanehori K., Takahashi-Fujii A., Oshima A., Sugiyama A.,  
 RA Kawakami B., Suzuki Y., Sugano S., Nagahari K., Masuho Y., Nagai K.,  
 RA Isogai T.;  
 RT "NEDO human cDNA sequencing project.";  
 RL Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.  
 DR EMBL; AK091977; BAC03783.1; -.  
 DR GO; GO:0016758; F:transferase activity, transferring hexosyl . . .; IEA.  
 DR GO; GO:0008152; P:metabolism; IEA.  
 DR InterPro; IPR002213; UDP\_gluco\_trans.  
 DR Pfam; PF00201; UDPGT; 1.  
 DR PROSITE; PS00375; UDPGT; 1.  
 KW Hypothetical protein.  
 SQ SEQUENCE 221 AA; 24764 MW; ACB59BEF47ACD458 CRC64;

Query Match 34.8%; Score 963; DB 4; Length 221;  
 Best Local Similarity 79.6%; Pred. No. 2.1e-72;  
 Matches 176; Conservative 21; Mismatches 24; Indels 0; Gaps 0;

Qy 303 MVNTCQNPEIFKEMNNAFAHLPQGVIWKCQCSHWPKDVHLLAANVKIVDWLPQSDLLAHPS 362  
 |:| | : | : |:|:||||||| || ||||:|||| | ||||| ||||| |||||  
 Db 1 MLNTHQSQEVLKKMHNAFAHLPQGVIWTCQSSHWPRDVHLATNVKIVDWLPQSDLLAHPS 60  
 Qy 363 IRLFVTHGGQNSIMEAIQHGVPMVGIPFGDQPENMVRVEAKKFGVSIQLKKLKAETIAL 422  
 ||||| |||||:||||:|||||:|: || | |||| || :|||:| :: |:| |  
 Db 61 IRLFVTHGGQNSVMEAIRHGVPMVGLPVNGDQHGNMVRVVAKNYGVSIIRLNQVTADTLTL 120  
 Qy 423 KMKQIMEDKRYKSAAVAASVILRSHPLSPTQRLVGWIDHVLQTGGATHLKPYVFQQPWHE 482  
 |||:|:||||| ||||| | |||| |||||:||||||| |||||



DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Hypothetical UDP-glucoronosyl and UDP-glucosyl transferase containing  
 DE protein.  
 GN AI313915.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=Aorta, and Vein;  
 RX MEDLINE=22354683; PubMed=12466851;  
 RA The FANTOM Consortium,  
 RA the RIKEN Genome Exploration Research Group Phase I & II Team;  
 RT "Analysis of the mouse transcriptome based on functional annotation of  
 RT 60,770 full-length cDNAs."  
 RL Nature 420:563-573(2002).  
 DR EMBL; AK041045; BAC30796.1; -.  
 DR MGD; MGI:2145969; AI313915.  
 DR GO; GO:0016758; F:transferase activity, transferring hexosyl . . .; IEA.  
 DR GO; GO:0008152; P:metabolism; IEA.  
 DR InterPro; IPR002213; UDP\_gluco\_trans.  
 DR Pfam; PF00201; UDPGT; 1.  
 KW Hypothetical protein.  
 SQ SEQUENCE 302 AA; 35256 MW; C78A84C1D58987DC CRC64;

Query Match 28.6%; Score 792; DB 11; Length 302;  
 Best Local Similarity 57.9%; Pred. No. 6.7e-58;  
 Matches 157; Conservative 37; Mismatches 75; Indels 2; Gaps 2;

Qy	1	MAGQRVLLLVGFLLPGVLLSEAAKILTISTVGGSHYLLMDRVSQILQDHGHNVTMLNHKR	60
		:     :           :    :   :        : :	
Db	1	MAAHRRWLMSFLFLEVILLEAAKILTISTLSASHYIVISRVSQVLHEGGHNVTKLLYES	60
Qy	61	GPFMPDFKKEEKSYQVISWLPEDHQREFKKSFDFFLEETLGGRGKFENLLNVLEYLALQ	120
		:    :   :     :       : :            : :	
Db	61	AN-IPDFRKEKPSYQVINWRPPEDQEKKFADLRHRLTEEITYGRSKHHTLLKIHQYFGDL	119
Qy	121	CSHFLENRKDIMDSLKNENFDMVIVETFDYCPFLIAEKLKGKPFVAILSTSFGLP-I	179
		:            :   : : :               :     : :	
Db	120	CSQLLSRKDIMDFLKNENFDLVLLDSMDLCSLLIVEKLGRFVSFLPFQFSYMDFGLP	179
Qy	180	PLSYVPVFRSLTDMDFWGRVKNFLMFFSFCRRQQHMQSTFDNTIKEHFTEGSRPVL	239
		:                     : : :   : :   :        :	
Db	180	PLSYAPVYGSGGLTDQMDFWGRVKNFLMFLDFSMKQREILSQYDSTIQEHFVEG	239
Qy	240	LLKAEWLFINSDFAFDFARPLLPNTVYVGG	270
		:	
Db	240	LLKAEWLFVNSDFALDFARPLFPNTVYVGG	270

# RESULT 9

Q98TB5

ID Q98TB5 PRELIMINARY; PRT; 541 AA.  
 AC Q98TB5;







Db 113 NCDMMVG NQALI QGLKKEKFDLLLVDPNDMCGFVIAHLLGVKYAVFSTGLWYP AEVGAPA 172

Qy 180 PLSYVPVFRSLLTDHMDFWGRVKN-----FLMFFSFCRRQQH-----MQSTFD 222  
 ||: || | |||| |: | |: || ||: : | | : | : |

Db 173 PLAYVPEFNSLLTDRMNF LERMKN TG VYLISRIGVSFLVLPKYERIMQKYNLLPAKSMYD 232

Qy 223 NTIKEHFTEGSRPVL SHLL LK AELWFINSDFAFDFARPLLNTVYVGG LMEKPIKPV PQD 282  
 | : : || : : | | : | || || | ||| : : || | : | :

Db 233 -----LVHGSSLWMLCTDVALEFP RPTLPNVVYVGGILTKPASPLPED 275

Qy 283 LENFIAKFGDSGFVLVTLGSMVNTCQNPEIFKEMNNAFAHLPQGV IWKCCSHWP KDVHL 342  
 | : :: : : |||| : | : : | : : | || ||| : : | : |

Db 276 LQRWVSGAQEHGFVLVSFGAGVKYL-SEDIANKLAGALGRLPQKV IWRFSGT---KPKNL 331

Qy 343 AANVKIVDWLPQSDLLAHP SIRLFVTHGGQNSIMEAIQHGVPMVGIPLFGDQ PENMVRVE 402  
 | | : : ||| : || | : || | : || | | : | ||| : |||| | : | || :

Db 332 GNNTKLIEWLPQNDLLGHSNIRAFLSHGGLNSIFETMYHGV PVVGIPLFGDHYDTMTRVQ 391

Qy 403 AKKFGVSIQLKKLKAETLALKMKQIMEDKRYKSAAVAASVILRSHPLSPTQRLVGWIDHV 462  
 || | : : : | : : : : | : | | : | | | ||| : :

Db 392 AKGMGILLEWNTVTEGELYDALVKVINNP SYRQRAQKLSEIHKDQPGHPVNRTTYWIDYI 451

Qy 463 LQTGGATHLKPYPVFQQPWHEQYLF DV-FVFL LGLTL 497  
 | : || || : | | : : : | | : || || |

Db 452 LRHDGARHLRS AVHQISFCQYFLLDIAFVLLLGAVL 487

# RESULT 11

## Q9TSL6

ID Q9TSL6 PRELIMINARY; PRT; 529 AA.

AC Q9TSL6;

DT 01-MAY-2000 (TrEMBLrel. 13, Created)

DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)

DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)

DE UDP-glucuronosyltransferase 2B23 (EC 2.4.1.17).

OS *Macaca fascicularis* (Crab eating macaque) (*Cynomolgus* monkey).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;

OC Cercopithecinae; *Macaca*.

OX NCBI\_TaxID=9541;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=20043918; PubMed=10579317;

RA Barbier O., Levesque E., Belanger A., Hum D.W.;

RT "UGT2B23, a novel uridine diphosphate-glucuronosyltransferase enzyme

RT expressed in steroid target tissues that conjugates androgen and

RT estrogen metabolites.";

RL Endocrinology 140:5538-5548(1999).

DR EMBL; AF112113; AAF14353.1; -.

DR GO; GO:0015020; F:glucuronosyltransferase activity; IEA.

DR GO; GO:0008152; P:metabolism; IEA.

DR InterPro; IPR002213; UDP\_gluco\_trans.

DR Pfam; PF00201; UDPGT; 1.

DR PROSITE; PS00375; UDPGT; 1.

KW Glycosyltransferase; Transferase.

SQ SEQUENCE 529 AA; 60957 MW; 646315E6D970541A CRC64;

Query Match 24.9%; Score 689.5; DB 6; Length 529;  
Best Local Similarity 32.1%; Pred. No. 5.5e-49;  
Matches 168; Conservative 85; Mismatches 205; Indels 65; Gaps 14;

Qy	34	SHYLLMDRVSQIILQDGHNVNMTL-----NH-----KRGPFMPDFKKEE-----KSYQ	75
Db	34	SHWMNMKTILEELVQRGHEVTALASSASILFDPNNSALKIEVFPTSLPKPEFENIVTQE	93
Qy	76	VISWL-APEDHQREFKKSFDFFLEETLGGRGKFENLLNVLEYLALQCSHFLNRKDIMDSL	134
Db	94	IKRWIELPKD-----TFWLIFSQMQEIMWKFGDIFRNF-----CKDVVSNNKKLMKKL	140
Qy	135	KNENFDMVIVETFDYCPFLIAEKLGPVFVAILSTSFGSLEF-----GLPIPLSY	183
Db	141	QESRFDVVFADPIFPCELLAELFNIPLVY-----SLRFTPGYVFEKHCGGFLFPSPY	193
Qy	184	VPVFRSLTLDHMDFWGRVKN--FLMFFSFCCRQQHMQSTFDNTIKEHFTE--GSRPVLSH	239
Db	194	VPVVMSELSDQMTFMERVKNMIYMLYFDFCFQIYDMKKW-----DQFYTEVLGRHTTLSE	248
Qy	240	LLLKAELWFINSDFAFDFARPLLNPNTVYVGGLMKEPIKVPVQDLENFIAKFGDSGFVLVT	299
Db	249	IMGKADIWLIRNSWNFQFPHPLLPNVDFIGGLLCKPAKPLPKEMEEFVQSSGENGVVFT	308
Qy	300	LGSMVNTCQNPEIFKEMNNAFAHLPQGVWKQCQSHWPKDVHLAANVKIVDWLPQSDLLA	359
Db	309	LGSMI-TNMKEERANVIASALAQIPQKVLWRFDGN---KPDTLGVNTRLYKWIPQNDLLG	364
Qy	360	HPSIRLFVTHGGQNSIMEAIQHGVPVVGPIPLFGDQPENMVRVEAKKFGVSIQLKKLKAET	419
Db	365	HPKTKAFITHGGANGIYEAIYHGVPVVGPIPLFADQPDNIAHMKTRGAAVQLDFDTMSSTD	424
Qy	420	LALKMKQIMEDKRYKSAAVAASVILRSHPLSPQRLVGWIDHVLQTTGGATHLKPYVFQQP	479
Db	425	LVNALKTVINDPLYKENVMKLSRIQRDQVPKPLDRAVFWIEFVMRHKGAKHLRPAADHDLT	484
Qy	480	WHEQYLFVDVFVFLGLTLGLTLWLCLGKLLGMAVWWLRGARKVKE	522
Db	485	WFOYHSFDVIGFLLACVATVIFIIMKCCLFCFW--KFARKGKK	525

## RESULT 12

097951

ID 097951 PRELIMINARY; PRT; 529 AA.

AC 097951;

DT 01-MAY-1999 (TrEMBLrel. 10, Created)

DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

DE UDP-glucuronosyltransferase.

GN UGT2B18.

OS *Macaca fascicularis* (Crab eating macaque) (*Cynomolpus* monkey).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;

OC Cercopithecinae; Macaca.

OX NCBI TaxID=9541;

RN [11]

RP SEQUENCE FROM N.A.

RA Beaulieu M., Levesque E., Barbier O., Turgeon D., Belanger G.,  
 RA Hum D.W., Belanger A.;  
 RL Submitted (JUL-1997) to the EMBL/GenBank/DDBJ databases.  
 DR EMBL; AF016310; AAC98726.1; -.  
 DR GO; GO:0016758; F:transferase activity, transferring hexosyl . . .; IEA.  
 DR GO; GO:0016740; F:transferase activity; IEA.  
 DR GO; GO:0008152; P:metabolism; IEA.  
 DR InterPro; IPR002213; UDP\_gluco\_trans.  
 DR Pfam; PF00201; UDPGT; 1.  
 DR PROSITE; PS00375; UDPGT; 1.  
 KW Transferase.  
 SQ SEQUENCE 529 AA; 60801 MW; 3ECEB497B8C3601F CRC64;

Query Match 24.8%; Score 685.5; DB 6; Length 529;  
 Best Local Similarity 33.2%; Pred. No. 1.2e-48;  
 Matches 173; Conservative 75; Mismatches 212; Indels 61; Gaps 14;

Qy	34	SHYLLMDRVSQILQDHGHNVTML-----NH----KRGPFMPDFKKEEKS----YQ	75
		: :   : :         :	
Db	34	SHWMNMKTILEELVQRGHEVTVLASSASILFDPNNSALKIEVFPTSLTKTEFENIIRQQ	93
Qy	76	VISWL-APEDHQREFKKSFDFFLEETLGGRGKFENLLNVLEYLALQCSHFLNRKDIMDSL	134
		:     :   : : :     : :   :	
Db	94	IKRWSELPKD-----TFWLIFSQMQEIMWKFGDITRNF-----CKDVVSNNKKLMKKL	140
Qy	135	KNENFDMVIVETFDYCPFLIAEKLKGFVAILSTSFGSLEF-----GLPIPLSY	183
		:     : :	
Db	141	QKSREDFVVFADAI FPCSELLAELLNTPLVY-----SLRFTPGYNFEKHCGGFLFPFSY	193
Qy	184	VPVFRSLLTDHMDFEWGRVKN--FLMFFSFCCRQOHMQSTFDNTIKEHFTEGSRPVLSHLL	241
		:               : :	
Db	194	VPVVMSELSDHMTFMERVKNMIYMLYDFDC-FQIYAMKKWDQFYSE--VLGRPTTLSETM	250
Qy	242	LKAELWFINSDFAFDFARPLLNPNTVYVGGLMKPKPKVPQDLENFIAKFGDSGFVLVTLG	301
		: :   : :           :         : :	
Db	251	GKADIWLIRNSWNFQFPHPLLPNVDFVGGHLCKPAKPLPKEMEETFVQSSGENGVVVFSLG	310
Qy	302	SMVNTCQNPEIFKEMNNAFAHLPQGVIWKCQC SHWPKDVHLAANVKIVDWLPQSDLLAHP	361
		: :     :     :     : :     :	
Db	311	SMV-TNMKEERANVIASALAIQPKVLWRFD---GKKPDTLGLNTRLYKWIPQNDLLGHP	366
Qy	362	SIRLFVTHGGQNSIMEAIQHGVPMVGIP LFGDQPENMVRVEAKKFGVSIQLKKLKAETLA	421
		:                           : :     : :	
Db	367	KTRAFITHGGSNGIYEAIYHGVP MVGIP LFADQPDNIAHMKAKGAAVRLDFDTMSSTD LV	426
Qy	422	LKMKQIMEDKRYKSAVAASVILRSHPLSPTQRLVGWIDHVLQTGGATHLKPYVFQQPWH	481
		:   : :     :       :         : :	
Db	427	NALKTVINDPLYKENVMKLSRIQHDQPVKPLDRAVFWIEFVMRHKGAKHLRPA AHDLTWF	486
Qy	482	EQYLFDFVVFLLGLTLGLTLWL CGKLLGMAVWWLRGARKVKE	522
		: :         : :     :	
Db	487	QYHSLDVIGFLLACVATVIFIIMKCCLFCFW--KFARKGKK	525

RESULT 13

Q8BWQ1

ID Q8BWQ1 PRELIMINARY; PRT; 534 AA.

AC Q8BWQ1;  
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Similar to UDP glucuronosyltransferase UGT2A3.  
 GN 2010321J07RIK.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=Liver;  
 RX MEDLINE=22354683; PubMed=12466851;  
 RA The FANTOM Consortium,  
 RA the RIKEN Genome Exploration Research Group Phase I & II Team;  
 RT "Analysis of the mouse transcriptome based on functional annotation of  
 RT 60,770 full-length cDNAs.";  
 RL Nature 420:563-573(2002).  
 DR EMBL; AK050327; BAC34191.1; -.  
 DR MGD; MGI:1919344; 2010321J07Rik.  
 DR GO; GO:0016758; F:transferase activity, transferring hexosyl . . .; IEA.  
 DR GO; GO:0008152; P:metabolism; IEA.  
 DR InterPro; IPR002213; UDP\_gluco\_trans.  
 DR Pfam; PF00201; UDPGT; 1.  
 DR PROSITE; PS00375; UDPGT; 1.  
 SQ SEQUENCE 534 AA; 61119 MW; 3BF4F591395B1620 CRC64;

Query Match 24.8%; Score 685.5; DB 11; Length 534;  
 Best Local Similarity 33.5%; Pred. No. 1.2e-48;  
 Matches 171; Conservative 83; Mismatches 195; Indels 61; Gaps 13;

Qy	34	SHYLLMDRVSQILQDHGHNVTMLNH-----KRGPFMPDFKKEEKSYQVIS	78
		:  : : :       :  : :   : : :   :	
Db	34	SHWLNKLTILEELGARGHEVTVLKYPSTIIDQSKRIPLHFENIPLLYEIEAENRLNEIA	93
Qy	79	WLA----PEDHQREFKKSF-DFFLEETLGGRGKFENLLNVLEYLALQCSHFLNRKDIMS	133
		:   :    :       : :     :	
Db	94	NLAVNVIPNLSLWEAAKTLDQDFLQVT----GDFESI-----CRSVLYNQKFMDK	139
Qy	134	LKNENFDMVIVETFDYCPFLIAEKLKGFVAILSTSFG---SLEFG-LPIPLSYVPVFRS	189
		: :  : : : :    :	
Db	140	LRDAQYDVVVIDPVVPCGELVAEVLQIPFVYTLRFSGMGYYMEKHCGQLPIPLSYVPVMS	199
Qy	190	LLTDHMDFWGRVKN--FLMFFSFCRRQOHMQSTFDNTIKEHF---TEGSRPVLSHLLLKA	244
		:          :   : :   :   :     :	
Db	200	ELTDNMTFTERVKNMMFSLLEFYWLQQ-----YDFAFDQFYSETLGRPTTFCKTVGKA	253
Qy	245	ELWFINSDFAFDFARPLLNTVYVGGLMKPKPKVPQDLENFIAKFGDSGFVLVTLGSMV	304
		: :   : : :          :          : : :   :   :   :	
Db	254	DIWLIRTYWDVEFRPYLPNFEEFVGGHLCKPAKPLPKEMEETFVQSSGEHGVVVSIGSMV	313
Qy	305	NTCQNPEIFKEMNNAFAHLPGQVIWKQCQSHWPKDVHLAANKIVDWLPQSDLLAHPSIR	364
		: :   :     :  :     :   : :  : :        :	
Db	314	KNL-TEEKANLIASVLAQIPQKVLWRYS---GKKPATLGSNTRLFNWIPQNDLLGHPKTK	369
Qy	365	LFVTHGGQNSIMEAIQHGVPMVGIPLFGDQPENMVRVEAKKFGVSIQLKKLKAETLALKM	424

```

      |:||| | | || | |||||:|: ||| |: :||| : : : : : | :
Db      370 AFITHGGTNGIYEAIYHGVPMVGVPMGLGDQPHNIAHMEAKGAALKVSISTMTSTDLLSAV 429

Qy      425 KQIMEDKRYKSAAVAASVILRSHPLSPTQRLVGWIDHVLQTTGGATHLKPYPVQQPWHEQY 484
      : : : | | |: | | |: | | ||: |: : | | |: | : :
Db      430 RAVINEPSYKENAMRLSRIHHDQPVKPLDRAVFWIEFVMRHKGAKHLRVAAHDLSWFQYH 489

Qy      485 LFDVVFVFL-----GLTLGTLWLCGKL 506
      || ||| :| |:| ||
Db      490 SLDVIGFLLLCVVTLTFTIITKFCLEVCQKL 519

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RESULT 14

Q9BDZ8

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ID      Q9BDZ8      PRELIMINARY;      PRT;      498 AA.
AC      Q9BDZ8;
DT      01-JUN-2001 (TrEMBLrel. 17, Created)
DT      01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT      01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE      UDP-galactose ceramide galactosyltransferase (EC 2.4.1.47)
DE      (Fragment).
GN      CGT.
OS      Bos taurus (Bovine).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC      Bovidae; Bovinae; Bos.
OX      NCBI_TaxID=9913;
RN      [1]
RP      SEQUENCE FROM N.A.
RA      Kapitonov D.;
RT      "Molecular cloning and expression of ceramide galactosyltransferases.
RT      Comparison with other glycosyltransferases.";
RL      Thesis (1997), Medical College of Virginia, Richmond, VA, USA.
RN      [2]
RP      SEQUENCE FROM N.A.
RA      Kapitonov D.;
RL      Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.
DR      EMBL; AF129810; AAK16235.1; -.
DR      GO; GO:0047263; F:N-acylsphingosine galactosyltransferase act. . . ; IEA.
DR      GO; GO:0016758; F:transferase activity, transferring hexosyl . . . ; IEA.
DR      GO; GO:0008152; P:metabolism; IEA.
DR      InterPro; IPR002213; UDP_gluco_trans.
DR      Pfam; PF00201; UDPGT; 1.
DR      PROSITE; PS00375; UDPGT; 1.
KW      Glycosyltransferase; Transferase.
FT      NON_TER      1      1
SQ      SEQUENCE      498 AA; 56674 MW; 83645A7079ACF582 CRC64;

```

```

Query Match      24.7%; Score 684.5; DB 6; Length 498;
Best Local Similarity 32.8%; Pred. No. 1.3e-48;
Matches 161; Conservative 92; Mismatches 173; Indels 65; Gaps 12;

Qy      58 HKRGPFMPDFKKEEKSYQVISWLAPEDHQ--REFKKSF-----DFFLEETL----GGRGK 106
      |:|| : | : :||:| : : | | |: : ||
Db      3 HERGHHTVFLRSEGRD-----IAPSNHYSLQRYPGIFNSTTSDAFLQSKMRNIFSGRLT 56

Qy      107 FENLLNVLEYLALQCSHFLNRKDIMDSLKNENFDMVIVETFDYCPFLIAEKLGPVFVAIL 166

```

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      ||::||: | : : || |||::|: | | ||| || :
Db      57 AIELLDILDHYTKSCDMMVGNHALIQGLKQENFDLLLVDPNDMCGFLIAHLLGVKYAVFS 116
Qy      167 STSFGSLEFGLPIPLSYVPVFRSLTDMDFWGRVKN-----FLMFFSFCRRQ 214
      : : | | | ||:| | | |||||: |:|| | | : |
Db      117 TGLWYPAEVGAPAPLAYVPEFNSLLTDHMNLLQRMKNTGVYLISRIGISFLVLPKYERIM 176
Qy      215 QHM-----QSTFDNTIKEHFTEGSRPVLSHLLLKAEWLFINSDFAFDFARPLLNTVYVG 269
      | : : | : : || : : | : | | | | | |
Db      177 QEYNLLPEKSMYD-----LVYGSSLWMLCTDVALEFPRTLPNVVYVG 219
Qy      270 GLMEKPIKVPVQDLENFIAKFGDSGFVLVTLGSMVNTCQNPEIFKEMNNAFAHLPQGVIV 329
      |:| || |:|:| : : : |||||: | : | : : | | | | |
Db      220 GILTKPASPLPEDFQRWVNGANEHGFVLVSFGAGVKYL-SEDIATKLAGALGRLPQKVIW 278
Qy      330 KCQCSHWPKDVHLAANVKIVDWLPQSDLLAHPSIRLFTVTHGGQNSIMEAIQHGVPVVGIP 389
      : : | : | : : |||||:| | : : |:| | | : | | | : | | |
Db      279 RFSGT---KPKNLGNTRLIEWLPQNDLLGHSNIKAFLSHGGLNSIFETMYHGVPVVGIP 335
Qy      390 LFGDQPENMVRVEAKKFGVSIQLKKLKAETLALKMKQIMEDKRYKSAAVAASVILRSHPL 449
      ||| : |:|:| | : : | : | : : : | : | | :
Db      336 LFGDHYDTMIRVQAKGMGILLEWKTVTEGELYEALVKVINNPYSYRQRAQKLSEIHKDQLR 395
Qy      450 SPTQRLVGWIDHVLQTTGGATHLKPYVFQQPWHEQYLED-VFVFLLG-----LTLGTLW 501
      | | | ||::|: || |:| | : : : | | ||| || | : | :
Db      396 HPVNRTVYWIDYILRHDGAHHIRAAVHQISFCQYFLLDIVFVLLLGAALFYFLLSWVTKF 455
Qy      502 LCGKLLGMAVW 512
      :| :: :|
Db      456 ICRRI--RSLW 464

```

# RESULT 15

Q9R110

```

ID   Q9R110          PRELIMINARY;          PRT;    530 AA.
AC   Q9R110;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   UDP glucuronosyltransferase UGT2A3.
OS   Cavia porcellus (Guinea pig).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
OX   NCBI_TaxID=10141;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Hartley; TISSUE=Liver;
RX   MEDLINE=99410697; PubMed=10479484;
RA   Smith S.A., Nagalla S.R., Andrews D.P., Olsen G.D.;
RT   "Morphine regulation of a novel uridine diphosphate glucuronosyl-
RT   transferase in guinea pig pups following in utero exposure.";
RL   Mol. Genet. Metab. 68:68-77(1999).
DR   EMBL; AF175221; AAD51732.1; -.
DR   GO; GO:0016758; F:transferase activity, transferring hexosyl . . .; IEA.
DR   GO; GO:0016740; F:transferase activity; IEA.
DR   GO; GO:0008152; P:metabolism; IEA.
DR   InterPro; IPR002213; UDP_gluco_trans.

```

DR Pfam; PF00201; UDPGT; 1.  
DR PROSITE; PS00375; UDPGT; 1.  
KW Transferase.  
SQ SEQUENCE 530 AA; 59895 MW; EE2F394D3FD484E1 CRC64;

Query Match 24.6%; Score 681; DB 11; Length 530;  
Best Local Similarity 32.2%; Pred. No. 2.9e-48;  
Matches 168; Conservative 88; Mismatches 227; Indels 38; Gaps 11;

```
Qy      13 LLPGVLLSEAAKILTISTVGG-----SHYLLMDRVSQILQDHGHNVTMLNHKR 60
      : || | | : | | | | | | | | | | | | | | | | | | | | | | |
Db      1 MAPGKLASAVLLLLCCAGSGFCGKVLVWPCEMSHWLNKLTLEELVKRGHEVTVLTLN 60

Qy     61 GPFMPDFKKEEKSQVISWLAPEHQREFKKSFDFFLEETL-----GGRGKFENL 110
      | : : : : | | | | | | | | | | | | | | | | | | | | | | |
Db     61 NLFIDYNRHPAFNFEVIP--VPTDKNMS-ENILNEFIELAVNVMPMTPLWQSGKLLQQFF 117

Qy    111 LNVLEYLALQCSHFLNRKDIMDSLKNENFDMVIVETFDYCPFLIAEKLKGKPFVAILSTSF 170
      : : | | | | : : : : | | : : | : : : : | | | | | | | | : | |
Db    118 VQITEDLGLNCRNTVYNQSLMKKLRDSKYDVLVTDVPVPCGELVAEMLGVFPVNMLKFSM 177

Qy    171 G-SLE---FGLPIPLSYVPVFRSLTDMDFWGRVKN--FLMFFSFCRRQQHMQSTFDNT 224
      | : : | | | | | | | | | | | | | | | | | | | | | | | | |
Db    178 GHTIEKYCGQLPAPPSYVPVPLGGLTTRMTFMERVKNMVFSVLFDWF-IQQYDYKFWQDF 236

Qy    225 IKEHFTEGSRPVLSHLLLKAELWFINSDFAFDFARPLLNTVYVGGLMEKPIKVPVQDLE 284
      | | | | : : | | | | : : | | | | : | | | | | | | | | | |
Db    237 YSEAL--GRPTTLCEIMGKAEIWLIRTYWDFEFPRPYLPNFEFVGGLHCKPAKPLPKEME 294

Qy    285 NFIKFGDSGFVLVTLGSMVNTCQNPEIFKEMNNAFAHLPQGVWKCQC SHWPKDVHLAA 344
      | : | : | : | | | | | | | | | | | | | | | | | | | | | |
Db    295 EFVQSSGEDGVVVFSLGSMVKNL-TEEKANLIASALAQIPQKVLWRYK---GKKPATLGP 350

Qy    345 NVKIVDWLPQSDLLAHPSIRLFVTHGGQNSIMEAIQHGVPMVGIPLFGDQPENMVRVEAK 404
      | : : | | : | | | | | | | | | | | | | | | | | | | | | |
Db    351 NTRLFDWIPQNDLLGHPKTKAFITHGGSNGIYEAIYHGVPMVGMPIFSDQPDNLAGMKAK 410

Qy    405 KFGVSIQLKKLKAETLALKMKQIMEDKRYKSAAVAASVILRSHPLSPTQRLVGWIDHVLQ 464
      | : : : : | : : : : | | | | : | | | | | | | | | | | |
Db    411 GAAVEVNMNTMTSADLLGALRTVINDPTYKENAMKLSRIHHDQPVKPLDRAAFWVEFVMH 470

Qy    465 TGGATHLKPYVFQQPWHEQYLFDFVFVFLGLTLGTLWLCGK 505
      || || : | : : || || | : | |
Db    471 HKGAKHLRVAHDLSWFAQYHSLDVIGFLLACVASAILLVTK 511
```

Search completed: May 7, 2004, 17:32:49  
Job time : 48 secs

OM protein - protein search, using sw model

Run on: May 7, 2004, 17:25:14 ; Search time 17 Seconds  
(without alignments)  
1601.923 Million cell updates/sec

Title: US-10-017-867A-282  
Perfect score: 2768  
Sequence: 1 MAGQRVLLLVGFLLPGVLLS.....GKLLGMAVWWLRGARKVKET 523

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_42:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	% Query		Match Length	DB	ID	Description
	Score	Match				
1	748.5	27.0	502	1	UDC1_RABIT	P36514 oryctolagus
2	699	25.3	541	1	CGT_HUMAN	Q16880 homo sapien
3	697	25.2	541	1	CGT_MOUSE	Q64676 mus musculu
4	684	24.7	541	1	CGT_RAT	Q09426 rattus norv
5	679	24.5	533	1	UD11_HUMAN	P22309 homo sapien
6	677.5	24.5	530	1	UDB2_RAT	P08541 rattus norv
7	673	24.3	530	1	UDBK_MACFA	O77649 macaca fasc
8	670	24.2	531	1	UDBD_RABIT	P36512 oryctolagus
9	669	24.2	535	1	UD11_MOUSE	Q63886 mus musculu
10	668	24.1	529	1	UDB1_RAT	P09875 rattus norv
11	665	24.0	531	1	UD15_RAT	Q64638 rattus norv
12	664.5	24.0	528	1	UDBJ_MACFA	Q9xt55 macaca fasc
13	663.5	24.0	529	1	UDB9_MACFA	O02663 macaca fasc
14	662.5	23.9	530	1	UDBE_RABIT	P36513 oryctolagus
15	661.5	23.9	528	1	UDB4_HUMAN	P06133 homo sapien
16	658	23.8	533	1	UD12_RAT	P20720 rattus norv
17	658	23.8	535	1	UD11_RAT	Q64550 rattus norv



18	657	23.7	530	1	UDBH_HUMAN	O75795	homo sapien
19	654.5	23.6	529	1	UDB7_HUMAN	P16662	homo sapien
20	651	23.5	527	1	UDA1_HUMAN	Q9y4x1	homo sapien
21	650	23.5	527	1	UDA1_RAT	P36510	rattus norv
22	649	23.4	523	1	UDBG_RABIT	O19103	oryctolagus
23	649	23.4	530	1	UDBF_HUMAN	P54855	homo sapien
24	642	23.2	528	1	UDBA_HUMAN	P36537	homo sapien
25	642	23.2	531	1	UD13_RAT	Q64637	rattus norv
26	639	23.1	530	1	UDB6_RAT	P19488	rattus norv
27	639	23.1	533	1	UD12_MOUSE	P70691	mus musculu
28	638.5	23.1	532	1	UD16_HUMAN	P19224	homo sapien
29	637.5	23.0	530	1	UDB5_MOUSE	P17717	mus musculu
30	636.5	23.0	529	1	UDBS_HUMAN	Q9by64	homo sapien
31	635	22.9	534	1	UD15_HUMAN	P35504	homo sapien
32	634	22.9	530	1	UDB3_RAT	P08542	rattus norv
33	632.5	22.9	530	1	UDBC_RAT	P36511	rattus norv
34	631	22.8	530	1	UD18_HUMAN	Q9haw9	homo sapien
35	629	22.7	520	1	UD17_MOUSE	Q62452	mus musculu
36	624.5	22.6	534	1	UD13_HUMAN	P35503	homo sapien
37	623.5	22.5	529	1	UDBB_HUMAN	O75310	homo sapien
38	623	22.5	531	1	UD17_RAT	Q64633	rattus norv
39	621	22.4	530	1	UD1A_HUMAN	Q9haw8	homo sapien
40	617	22.3	530	1	UD18_RAT	Q64634	rattus norv
41	615.5	22.2	532	1	UD14_RABIT	Q28612	oryctolagus
42	614	22.2	530	1	UD12_HUMAN	P36509	homo sapien
43	612	22.1	530	1	UD17_HUMAN	Q9haw7	homo sapien
44	612	22.1	530	1	UD19_HUMAN	O60656	homo sapien
45	611.5	22.1	531	1	UD16_MOUSE	Q64435	mus musculu

# ALIGNMENTS

## RESULT 1

### UDC1\_RABIT

ID UDC1\_RABIT STANDARD; PRT; 502 AA.  
AC P36514;  
DT 01-JUN-1994 (Rel. 29, Created)  
DT 01-JUN-1994 (Rel. 29, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE UDP-glucuronosyltransferase 2C1 microsomal (EC 2.4.1.17) (UDPGT)  
DE (Fragment).  
GN UGT2C1 OR UGT2A2.  
OS Oryctolagus cuniculus (Rabbit).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.  
OX NCBI\_TaxID=9986;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=New Zealand white; TISSUE=Liver;  
RX MEDLINE=93315511; PubMed=8325897;  
RA Tukey R.H., Pendurthi U.R., Nguyen N.T., Green M.D., Tephly T.R.;  
RT "Cloning and characterization of rabbit liver UDP-  
RT glucuronosyltransferase cDNAs. Developmental and inducible expression  
RT of 4-hydroxybiphenyl UGT2B13.";  
RL J. Biol. Chem. 268:15260-15266(1993).  
CC -!- FUNCTION: UDPGT is of major importance in the conjugation and

CC subsequent elimination of potentially toxic xenobiotics and  
 CC endogenous compounds.  
 CC -!- CATALYTIC ACTIVITY: UDP-glucuronate + acceptor = UDP + acceptor  
 CC beta-D-glucuronoside.  
 CC -!- SUBCELLULAR LOCATION: Microsomal.  
 CC -!- SIMILARITY: Belongs to the UDP-glycosyltransferase family.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL; L01083; AAA18023.1; -.  
 DR InterPro; IPR002213; UDP\_gluco\_trans.  
 DR Pfam; PF00201; UDPGT; 1.  
 DR PROSITE; PS00375; UDPGT; 1.  
 KW Transferase; Glycosyltransferase; Glycoprotein; Transmembrane;  
 KW Multigene family; Microsome.  
 FT NON\_TER 1 1  
 FT TRANSMEM 466 481 POTENTIAL.  
 FT CARBOHYD 177 177 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 288 288 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SQ SEQUENCE 502 AA; 57449 MW; B6E65670BFAE1D35 CRC64;

Query Match 27.0%; Score 748.5; DB 1; Length 502;  
 Best Local Similarity 35.4%; Pred. No. 3.4e-51;  
 Matches 180; Conservative 82; Mismatches 178; Indels 69; Gaps 14;

Qy 34 SHYLLMDRVSQILQDHGHNV-----MLNHKRGPFMPDFKK-----EE----- 71  
 ||::: : : : || || :| :|:| : || : : ||  
 Db 7 SHWINLKVILEELQLRGHEITVLPSPSLLLDHTKIPFNVEVLQLQVTKETLMEELNTVL 66  
 Qy 72 --KSYQV--ISWLAPEDHQREFKKSFDFFLEETLGGRGKFENLLNVLEYLALQCSHFLENR 127  
 |::: :|| | | | :|| | | :  
 Db 67 YMSSFELPTLSWWKVLGKMVEMGKQFS-----KNLRRV-----CDSAITSN 106  
 Qy 128 KDIMDSLKNENFDMVIVETFDYCPFLIAEKLKGKPFVAILSTSFGSLE----FGLPIPLSY 183  
 |:::| || ||: : : :| |::| | || |:: | || | ||  
 Db 107 KELLDRLKAAKFDICLADPLAFCELGELVAELNIPFVYSFRFSIGNIERSCAGLPTPSSY 166  
 Qy 184 VPFVRSLLTDHMDFWGRVKNFLMFFSFCRRQQH-MQSTFDNTIKEHFTE--GSRPVLSHL 240  
 || | ||:| | |::|::: | | :| |::: | | : :  
 Db 167 VPGSTSGLTDNMSFVQRLKNWLLYLMNDMMFSHFMLSEWD----EYYSKVLGRRTTICEI 222  
 Qy 241 LLKAELWFINSDFAFDFARPLLNTVYVGGLMEKPIKVPQDLENFIAKFGDSGFVLVTL 300  
 : ||::| | | : |::| | || | || | |::|::| | : | : | : ||  
 Db 223 MGKAEMWLIRSYWDFEFPRPFLPNFEYVGGLHCKPAKPLPEELEEFVQSSGNDGVVVFTL 282  
 Qy 301 GSMVNTCQNPEIFKEMNN---AFAHLPQGVWIKCQCSHWPKDVHLAANVKIVDWLPQSD 356  
 ||:: | | : :| :| | :|| |:: | | | : : :|::|  
 Db 283 GSMI---QN--LTEERSNLIASALAQIPQKVLWRYT---GKKPATLGPNTRLFEPQND 334  
 Qy 357 LLAHPSIRLFVTHGGQNSIMEAIQHGVPMVGIPLEFGDQPENMVRVEAKKFGVSIQLKKLK 416  
 || || | |::|| | : || | ||||| ||::|::| | : | : :

Db 335 LLGHPKTRAFITHGGTNGLYEAIYHGVPMVGIPLEFGDQPDNIARVKAKGAADVVDLRIMT 394

Qy 417 AETLALKMKQIMEDKRYKSAAVAASVILRSHPLSPTQRLVGWIDHVLQTGGATHLKPYPVF 476  
 :| :| :: : || |: | | || | | |:: |: : || |:

Db 395 TSSLLKALKDVINNPSYKENAMKLSRIHHDQPLKPLDRAVFWIEFVMRHKGARHLRVAAH 454

Qy 477 QQPWHEQYLFDFVFLGLTLGLTLWLCCGK 505  
 | : | || ||| : : | |

Db 455 DLTWFQYYSLDVVFLTCVATIIFLAKK 483

## RESULT 2

### CGT\_HUMAN

ID CGT\_HUMAN STANDARD; PRT; 541 AA.

AC Q16880; O00196;

DT 01-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE 2-hydroxyacylsphingosine 1-beta-galactosyltransferase precursor

DE (EC 2.4.1.45) (UDP-galactose-ceramide galactosyltransferase) (Ceramide

DE UDP-galactosyltransferase) (Cerebroside synthase).

GN UGT8 OR CGT OR UGT4.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI\_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=96299661; PubMed=8661025;

RA Bosio A., Binczek E., Lebeau M.M., Fernald A.A., Stoffel W.;

RT "The human gene CGT encoding the UDP-galactose ceramide galactosyl

RT transferase (cerebroside synthase): cloning, characterization, and

RT assignment to human chromosome 4, band q26.";

RL Genomics 34:69-75(1996).

RN [2]

RP SEQUENCE FROM N.A.

RX MEDLINE=97242209; PubMed=9125199;

RA Kapitonov D.E., Yu R.K.;

RT "Cloning, characterization, and expression of human ceramide

RT galactosyltransferase cDNA.";

RL Biochem. Biophys. Res. Commun. 232:449-453(1997).

CC -!- FUNCTION: CATALYZES THE TRANSFER OF GALACTOSE TO CERAMIDE, A KEY

CC ENZYMATIC STEP IN THE BIOSYNTHESIS OF GALACTOCEREBROSIDES, WHICH

CC ARE ABUNDANT SPHINGOLIPIDS OF THE MYELIN MEMBRANE OF THE CENTRAL

CC NERVOUS SYSTEM AND PERIPHERAL NERVOUS SYSTEM.

CC -!- CATALYTIC ACTIVITY: UDP-galactose + 2-(2-hydroxyacyl)sphingosine =

CC UDP + 1-(beta-D-galactosyl)-2-(2-hydroxyacyl)sphingosine.

CC -!- PATHWAY: Galactocerebroside biosynthesis.

CC -!- SIMILARITY: Belongs to the UDP-glycosyltransferase family.

CC -----

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CC -----  
 DR EMBL; U30930; AAC50565.1; -.  
 DR EMBL; U32370; AAC50815.1; -.  
 DR EMBL; U31353; AAC50815.1; JOINED.  
 DR EMBL; U31461; AAC50815.1; JOINED.  
 DR EMBL; U31658; AAC50815.1; JOINED.  
 DR EMBL; U31861; AAC50815.1; JOINED.  
 DR EMBL; U62899; AAC51187.1; -.  
 DR Genew; HGNC:12555; UGT8.  
 DR MIM; 601291; -.  
 DR GO; GO:0008489; F:UDP-galactose-glucosylceramide beta-1,4-gal. . .; TAS.  
 DR GO; GO:0007417; P:central nervous system development; TAS.  
 DR GO; GO:0007422; P:peripheral nervous system development; TAS.  
 DR InterPro; IPR002213; UDP\_gluco\_trans.  
 DR Pfam; PF00201; UDPGT; 1.  
 DR PROSITE; PS00375; UDPGT; 1.  
 KW Transferase; Glycosyltransferase; Glycoprotein; Transmembrane; Signal;  
 KW Microsome.  
 FT SIGNAL 1 20 POTENTIAL.  
 FT CHAIN 21 541 2-HYDROXYACYLSPHINGOSINE 1-BETA-  
 FT GALACTOSYLTRANSFERASE.  
 FT TRANSMEM 472 492 POTENTIAL.  
 FT CARBOHYD 78 78 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 333 333 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 442 442 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CONFLICT 99 99 T -> P (IN REF. 2).  
 FT CONFLICT 116 116 L -> M (IN REF. 2).  
 FT CONFLICT 356 356 L -> V (IN REF. 2).  
 FT CONFLICT 379 379 L -> V (IN REF. 2).  
 SQ SEQUENCE 541 AA; 61455 MW; EC532798F7E15834 CRC64;

Query Match 25.3%; Score 699; DB 1; Length 541;  
 Best Local Similarity 32.2%; Pred. No. 2.9e-47;  
 Matches 166; Conservative 95; Mismatches 185; Indels 70; Gaps 12;

Qy 13 LLPGVLLSEAAKILTISTV-GGSHYLLMDRVSQILQDHGHN-VTMLNHKRGPFMPDFKKE 70  
 | | ::|||: : : || : :: | : ||: | :: |  
 Db 11 LWSAVGIKAAKIIIVPPIMFESHMYIFKTLASALHERGHHTVFLLEGRD----- 61  
 Qy 71 EKSYQVISWLAPEDHQ--REFKKSF-----DFFLEETL----GGRGKFENLLNVLEYLAL 119  
 :|| :| : : | ||: : || | :::  
 Db 62 -----IAPSNHYSLQRYPGIFNSTTSDAFLQSKMRNIFSGRLTAIELFDILDHYTK 112  
 Qy 120 QCSHFLNRKDIMDSLKNENFDMVIVETFDYCPFLIAEKLKGKPFVAILSTSFGLSLEFGLPI 179  
 | : :: || | ||::|: | | || | | : : | | |  
 Db 113 NCDLMVGNHALIQLKKEKFDLLLVDPNDMCGFVIAHLLGVKYAVFSTGLWYPAEVGAPA 172  
 Qy 180 PLSYVPVFRSLLTDHMDFWGRVKN-----FLMFFSFCRRQQHM-----QSTFD 222  
 ||:|| | |||| | : | :|| ||: : | | : : |  
 Db 173 PLAYVPEFNSLLTDRMNLQRMKNTGVYLISRLGVSVFLVLPKYERIMQKYNLLPEKSMYD 232  
 Qy 223 NTIKEHFTGSRPVLSHLLLKAEWLFINSDFAFDFAFARPLLNTVYVGGIMEKPIKVPVQD 282  
 | : : || : : | : | || || | |||:: || | :| :|  
 Db 233 -----LVHGSSLWMLCTDVALEFPRLPNVYVGGILTTPASPLPED 275  
 Qy 283 LENFIAKFGDSGFVLVTLGSMVNTCQNPEIFKEMNNAFAHLPQGVWKCQCSHWPKDVHL 342  
 | : : : ||||: | : | : : | || ||| : || :|

Db 276 LQRWVNGANEHGFVLVSFGAGVKYL-SEDIANKLAGALGRLPQKVIWRFS---GPKPKNL 331

Qy 343 AANVKIVDWLPQSDLLAHPSIRLFVTHGGQNSIMEAIQHGVPVVGIPPLFGDQPENMVRVE 402  
 | |::|||:| | | |::|| | | : |||:||||| : | ||:

Db 332 GNNTKLIEWLPQNDLLGHGSKIKAFLSHGGLNSIFETMYHGVPPVVGIPPLFGDHYDTMTRVQ 391

Qy 403 AKKFGVSIQLKKLKAETLALKMKQIMEDKRYKSAAVAASVILRSHPLSPTQRLVGVWIDHV 462  
 || |::| : : | : :: : | : | | : | | : ||::

Db 392 AKGMGILLEWKTVTTEKELYEALVKVINNPYSYRQRAQKLSEIHKDQPGHPVNRTIYWIDYI 451

Qy 463 LQTGGATHLKPYVFQQPWHEQYLFQDV-FVFLGLTL 497  
 :: || ||: | | : : : | : || || |

Db 452 IRHNGAHLRAAVHQISFCQYFLDIAFVLLIGAAL 487

### RESULT 3

#### CGT\_MOUSE

ID CGT\_MOUSE STANDARD; PRT; 541 AA.

AC Q64676; Q61634;

DT 01-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE 2-hydroxyacylsphingosine 1-beta-galactosyltransferase precursor

DE (EC 2.4.1.45) (UDP-galactose-ceramide galactosyltransferase) (Ceramide

DE UDP-galactosyltransferase) (Cerebroside synthase).

GN UGT8 OR CGT OR UGT4.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI\_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=BALB/c;

RA Bosio A., Binczek E., Stoffel W.;

RL Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases.

RN [2]

RP SEQUENCE FROM N.A.

RA Coetzee T., Li X., Fujita N., Marcus J., Suzuki K., Francke U.,

RA Popko B.;

RL Submitted (FEB-1996) to the EMBL/GenBank/DDBJ databases.

CC -!- FUNCTION: CATALYZES THE TRANSFER OF GALACTOSE TO CERAMIDE, A KEY

CC ENZYMATIC STEP IN THE BIOSYNTHESIS OF GALACTOCEREBROSIDES, WHICH

CC ARE ABUNDANT SPHINGOLIPIDS OF THE MYELIN MEMBRANE OF THE CENTRAL

CC NERVOUS SYSTEM AND PERIPHERAL NERVOUS SYSTEM.

CC -!- CATALYTIC ACTIVITY: UDP-galactose + 2-(2-hydroxyacyl)sphingosine =

CC UDP + 1-(beta-D-galactosyl)-2-(2-hydroxyacyl)sphingosine.

CC -!- PATHWAY: Galactocerebroside biosynthesis.

CC -!- SIMILARITY: Belongs to the UDP-glycosyltransferase family.

CC -----

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CC -----

DR EMBL; X92122; CAA63090.1; -.  
 DR EMBL; X92123; CAA63091.1; -.  
 DR EMBL; X92124; CAA63091.1; JOINED.  
 DR EMBL; X92125; CAA63091.1; JOINED.  
 DR EMBL; X92126; CAA63091.1; JOINED.  
 DR EMBL; X92177; CAA63091.1; JOINED.  
 DR EMBL; U48896; AAC53576.1; -.  
 DR EMBL; U48892; AAC53576.1; JOINED.  
 DR EMBL; U48893; AAC53576.1; JOINED.  
 DR EMBL; U48894; AAC53576.1; JOINED.  
 DR MGD; MGI:109522; Ugt8.  
 DR InterPro; IPR002213; UDP\_gluco\_trans.  
 DR Pfam; PF00201; UDPGT; 1.  
 DR PROSITE; PS00375; UDPGT; 1.  
 KW Transferase; Glycosyltransferase; Glycoprotein; Transmembrane; Signal;  
 KW Microsome.  
 FT SIGNAL 1 20 POTENTIAL.  
 FT CHAIN 21 541 2-HYDROXYACYLSPHINGOSINE 1-BETA-  
 FT GALACTOSYLTRANSFERASE.  
 FT TRANSMEM 472 492 POTENTIAL.  
 FT CARBOHYD 78 78 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 333 333 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 442 442 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CONFLICT 335 335 T -> S (IN REF. 2).  
 FT CONFLICT 458 458 H -> R (IN REF. 2).  
 FT CONFLICT 511 511 K -> E (IN REF. 2).  
 FT CONFLICT 524 524 P -> R (IN REF. 2).  
 FT CONFLICT 533 534 HI -> RV (IN REF. 2).  
 FT CONFLICT 541 541 K -> R (IN REF. 2).  
 SQ SEQUENCE 541 AA; 61137 MW; B76F80A9B5326EE8 CRC64;

Query Match 25.2%; Score 697; DB 1; Length 541;  
 Best Local Similarity 32.4%; Pred. No. 4.2e-47;  
 Matches 167; Conservative 95; Mismatches 184; Indels 70; Gaps 12;

Qy 13 LLPGVLLSEAAKILTISTV-GGSHYLLMDRVSQILQDHGHN-VTMLNHKRGPFMPDFKKE 70  
 | | :: ||| : : : | | : : : | : || : | : | : |  
 Db 11 LWSAVGIARAAKIIIVPPIMFESHLYIFKTLASALHERGHHTVLLLEGRD----- 61  
 Qy 71 EKSQVISWLAPEDHQ--REFKKSF-----DFFLEETL----GGRGKFENLLNVLEYLAL 119  
 : || : | : : | | || : : || | : : : :  
 Db 62 -----IAPSNHYSLQRYPGIFNSTTSDAFLQSKMRNIFSGRLTAVELVDILDHYTK 112  
 Qy 120 QCSHFLNRKDIMDSLKNENFDMVIVETFDYCPFLIAEKLKGKPFVAILSTSFGSLEFGLPI 179  
 | : : : : || | || : : : | | | : || | : : : | | |  
 Db 113 NCDMMVGNQALIQGLKKEKFDLLLVDPNDMCGFVIAHLLGVKYAVFSTGLWYPAEVGAPA 172  
 Qy 180 PLSYVPVFRSLLTDHMDFWGRVKN-----FLMFFSFCCRQOH-----MQSTFD 222  
 || : || | | || | | : | | : || : : | | : | : |  
 Db 173 PLAYVPEFNSLLTDRMNFLERMKNTGVYLISRIGVSFLVLPKYERIMQKYNLLPAKSMYD 232  
 Qy 223 NTIKEHFTEGSRPVLSHLLLKAELWFINSDFAFDFARPLLNTVYVGGIMEKPIKVPVQD 282  
 | : : || : : | | : | || || | || | : : || | : : |  
 Db 233 -----LVHGSSLWMLCTDVALEFPRTLPNVVYVGGILTTPASPLPED 275  
 Qy 283 LENFIAKFGDSGFVLVTLGSMVNTCQNPEIFKEMNNAFAHLPQGVWKCQCSHWPKDVHL 342  
 | : : : : | || | : | : : | : : | || | : : | : |

Db	276	LQRWVSGAQEHGFVLVSFGAGVKYL-SEDIANKLAGALGRLPQKVIWRFSGT---- <td>331</td>	331
Qy	343	AANVKIVDWLPQSDLLAHPSIRLFVTHGGQNSIMEAIQHGVPMVGIPLFQDQOPENMVRVE	402
		: ::     :      :      :        :       :        :	
Db	332	GNNTKLI EWLPQNDLLGHSNIRAFLSHGGLNSIFETMYHGVPPVGIPLFQGDHYDTMTRVQ	391
Qy	403	AKKFGVSIQLKKLKAETLALKMKQIMEDKRYKSAAVAASVILRSHPLSPTQRLVGWIDHV	462
		: :: :   : :: :   :     :           ::	
Db	392	AKGMGILLEWNTVTEGELYDALVKVINNPYSYRQRAQKLSEIHKDQPGHPVNRTTYWIDYI	451
Qy	463	LQTGGATHLKPYPVFPWHEQYLFQDV-FVFLGLTL	497
		:       :     : : :     :	
Db	452	LRHDGAHHLRSVHQSFCQYFLLDIAFVLLLGAVL	487

## RESULT 4

## CGT RAT

```

ID      CGT_RAT          STANDARD;          PRT;      541 AA.
AC      Q09426;
DT      01-NOV-1995 (Rel. 32, Created)
DT      01-NOV-1995 (Rel. 32, Last sequence update)
DT      28-FEB-2003 (Rel. 41, Last annotation update)
DE      2-hydroxyacylsphingosine 1-beta-galactosyltransferase precursor
DE      (EC 2.4.1.45) (UDP-galactose-ceramide galactosyltransferase) (Ceramide
DE      UDP-galactosyltransferase) (Cerebroside synthase).
GN      UGT8 OR CGT OR UGT4.
OS      Rattus norvegicus (Rat).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX      NCBI_TaxID=10116;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=Wistar; TISSUE=Brain;
RX      MEDLINE=94052143; PubMed=7694285;
RA      Schulte S., Stoffel W.;
RT      "Ceramide UDPgalactosyltransferase from myelinating rat brain:
RT      purification, cloning, and expression.";
RL      Proc. Natl. Acad. Sci. U.S.A. 90:10265-10269(1993).
RN      [2]
RP      SEQUENCE FROM N.A.
RC      STRAIN=Sprague-Dawley; TISSUE=Brain;
RX      MEDLINE=94358923; PubMed=7521399;
RA      Stahl N., Jurevics H., Morell P., Suzuki K., Popko B.;
RT      "Isolation, characterization, and expression of cDNA clones that
RT      encode rat UDP-galactose: ceramide galactosyltransferase.";
RL      J. Neurosci. Res. 38:234-242(1994).
CC      -!- FUNCTION: CATALYZES THE TRANSFER OF GALACTOSE TO CERAMIDE, A KEY
CC      ENZYMATIC STEP IN THE BIOSYNTHESIS OF GALACTOCEREBROSIDES, WHICH
CC      ARE ABUNDANT SPHINGOLIPIDS OF THE MYELIN MEMBRANE OF THE CENTRAL
CC      NERVOUS SYSTEM AND PERIPHERAL NERVOUS SYSTEM.
CC      -!- CATALYTIC ACTIVITY: UDP-galactose + 2-(2-hydroxyacyl)sphingosine =
CC      UDP + 1-(beta-D-galactosyl)-2-(2-hydroxyacyl)sphingosine.
CC      -!- PATHWAY: Galactocerebroside biosynthesis.
CC      -!- TISSUE SPECIFICITY: BRAIN, RESTRICTED TO THE OLIGODENDROCYTE-
CC      CONTAINING CELL LAYERS OF CEREBRUM AND CEREBELLUM.
CC      -!- SIMILARITY: Belongs to the UDP-glycosyltransferase family.
CC      -----

```

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 CC -----

DR EMBL; L21698; AAA16108.1; -.  
 DR EMBL; U07683; AAA50212.1; -.  
 DR PIR; A48801; A48801.  
 DR InterPro; IPR002213; UDP\_gluco\_trans.  
 DR Pfam; PF00201; UDPGT; 1.  
 DR PROSITE; PS00375; UDPGT; 1.  
 KW Transferase; Glycosyltransferase; Glycoprotein; Transmembrane; Signal;  
 KW Microsome.  
 FT SIGNAL 1 20 POTENTIAL.  
 FT CHAIN 21 541 2-HYDROXYACYLSPHINGOSINE 1-BETA-  
 FT GALACTOSYLTRANSFERASE.  
 FT TRANSMEM 472 492 POTENTIAL.  
 FT CARBOHYD 78 78 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 333 333 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 442 442 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SQ SEQUENCE 541 AA; 61126 MW; 260D7603170151BB CRC64;

Query Match 24.7%; Score 684; DB 1; Length 541;  
 Best Local Similarity 32.2%; Pred. No. 4.4e-46;  
 Matches 165; Conservative 94; Mismatches 184; Indels 70; Gaps 12;

Qy 13 LLPGVLLSEAAKILTISTV-GGSHYLLMDRVSQILQDHGHN-VTMLNHKRGPFMPDFKKE 70  
 | | :: ||| : : | | : : | : || : | : |  
 Db 11 LWSAVGIARAAKIIIVPPIMFESHLYIFKTLASALHERGHHTVFLLEGRD----- 61  
 Qy 71 EKSQYVISWLAPEDHQ--REFKKSF-----DFFLEETL----GGRGKFENLLNVLEYLAL 119  
 : | : | : : | | | : : | | : : : : : :  
 Db 62 -----IDPSNHYSLQRYPGIFNSTTSDAFLQSKMRNIFSGRLTAVELVDILDHYTK 112  
 Qy 120 QCSHFLENRKDIMDSLKNENFDMVIVETFDYCPFLIAEKLKGKPFVAILSTSEFGSLEFGLPI 179  
 | : : : : || | || : : : | | : | | : : : | | |  
 Db 113 NCDMMVGNQALIQGLKKEKFDLLLVDPNDMCGFVIAHLLGVKYAVFSTGLWYPAEVGAPA 172  
 Qy 180 PLSYVPVFRSILTDHMDFWGRVKN-----FLMFFSFCRRQQH-----MQSTFD 222  
 || : || | | || || : | | : || : : | | : | : |  
 Db 173 PLAYVPEFNSLLTDRMNFLERMKNTGVYLISRMGVSFLVLPKYERIMQKYNLLPAKSMYD 232  
 Qy 223 NTIKEHFTGSRPVLSHLLLKAELWFINSDFAFDFARPLLNTVYVGGLMKPKIPVPQD 282  
 | : : || : : | | : | | || | || || : : | | : | : |  
 Db 233 -----LVHGSSLWMLCTDVALEFPRPTLPNVVYVGGILTKPASPLPED 275  
 Qy 283 LENFIAKFGDSGFVLVTLGSMVNTCQNPEIFKEMNNAFAHLPQGVIWKCQCShwPKDVHL 342  
 | : : : : || || : | : : : | : | | | : : : | : |  
 Db 276 LQRWVDGAQEHEGFVLVSFGAGVKYL-SEDIANKLAGALGRLPQKVIWRFSGT---KPKNL 331  
 Qy 343 AANVKIVDWLPQSDLLAHPSIRLFVTHGGQNSIMEAIQHGVPVVGIPFGDQPENMVRVE 402  
 | | : : || || : || | : || | : || || | : || || : || || || : | || :  
 Db 332 GNNTKLI EWLPQNDLLGHSNIRAFLSHGGLNSIFETMYHGVVVGIPFGDHYDTMTRVQ 391



Qy 403 AKKFGVSIQLKKLKAETLALKMKQIMEDKRYKSAAVAASVILRSHPLSPTQRLVGWIDHV 462  
 || |: :: : | : :: : |: | | : | | | ||::  
 Db 392 AKGMGILLEWNTVTEGELYDALVKVINNPSYRQRAQKLSEIHKDQPGHPVNRTTYWIDYI 451  
 Qy 463 LQTGGATHLKPYVFQQPWHEQYLFDV-FVFLLG 494  
 |: || |: | | : : :| |: || |||  
 Db 452 LRHDGAHHLRSVHQISFCQYFLLDIAFVLLLG 484

# RESULT 5

## UD11\_HUMAN

ID UD11\_HUMAN STANDARD; PRT; 533 AA.  
 AC P22309;  
 DT 01-AUG-1991 (Rel. 19, Created)  
 DT 01-AUG-1991 (Rel. 19, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE UDP-glucuronosyltransferase 1-1 precursor, microsomal (EC 2.4.1.17)  
 DE (UDP-glucuronosyltransferase 1A1) (UDPGT) (UGT1\*1) (UGT1-01) (UGT1.1)  
 DE (UGT-1A) (UGT1A) (Bilirubin specific UDPGT isozyme 1) (HUG-BR1).  
 GN UGT1A1 OR UGT1 OR GNT1.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Liver;  
 RX MEDLINE=91093210; PubMed=1898728;  
 RA Ritter J.K., Crawford J.M., Owens I.S.;  
 RT "Cloning of two human liver bilirubin UDP-glucuronosyltransferase  
 RT cDNAs with expression in COS-1 cells."  
 RL J. Biol. Chem. 266:1043-1047(1991).  
 RN [2]  
 RP SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.  
 RX MEDLINE=92147680; PubMed=1339448;  
 RA Ritter J.K., Chen F., Sheen Y.Y., Tran H.M., Kimura S., Yeatman M.T.,  
 RA Owens I.S.;  
 RT "A novel complex locus UGT1 encodes human bilirubin, phenol, and  
 RT other UDP-glucuronosyltransferase isozymes with identical carboxyl  
 RT termini."  
 RL J. Biol. Chem. 267:3257-3261(1992).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=21327373; PubMed=11434514;  
 RA Gong Q.H., Cho J.W., Huang T., Potter C., Gholami N., Basu N.K.,  
 RA Kubota S., Carvalho S., Pennington M.W., Owens I.S., Popescu N.C.;  
 RT "Thirteen UDP-glucuronosyltransferase genes are encoded at the human  
 RT UGT1 gene complex locus."  
 RL Pharmacogenetics 11:357-368(2001).  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RA Gattung S., Stoneking T., Davidson T.;  
 RL Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.  
 RN [5]  
 RP SEQUENCE OF 1-50 FROM N.A.  
 RA Ueyama H., Koiwai O., Soeda Y., Sato H., Satoh Y., Ohkubo I.,  
 RA Doida Y.;

RT "Analysis of the promoter of human bilirubin  
 RT UDP-glucuronosyltransferase gene (UGT1\*1) in relevance to Gilbert's  
 RT syndrome.";  
 RL Hepatol. Res. 9:152-163(1997).  
 RN [6]  
 RP VARIANT CN-I PHE-375.  
 RX MEDLINE=92339803; PubMed=1634050;  
 RA Bosma P.J., Chowdhury J.R., Huang T.-J., Lahiri P., Elferink R.P.J.O.,  
 RA van Es H.H.G., Lederstein M., Whittington P.F., Jansen P.L.M.,  
 RA Chowdhury N.R.;  
 RT "Mechanisms of inherited deficiencies of multiple UDP-  
 RT glucuronosyltransferase isoforms in two patients with Crigler-Najjar  
 RT syndrome, type I.";  
 RL FASEB J. 6:2859-2863(1992).  
 RN [7]  
 RP VARIANTS CN-II ARG-71 AND ASP-486.  
 RX MEDLINE=94107323; PubMed=8280139;  
 RA Aono S., Yamada Y., Keino H., Hanada N., Nakagawa T., Sasaoka Y.,  
 RA Yazawa T., Sato H., Koiwai O.;  
 RT "Identification of defect in the genes for bilirubin UDP-glucuronosyl-  
 RT transferase in a patient with Crigler-Najjar syndrome type II.";  
 RL Biochem. Biophys. Res. Commun. 197:1239-1244(1993).  
 RN [8]  
 RP VARIANT CN-II ARG-331.  
 RX MEDLINE=94102756; PubMed=8276413;  
 RA Moghrabi N., Clarke D.J., Boxer M., Burchell B.;  
 RT "Identification of an A-to-G missense mutation in exon 2 of the UGT1  
 RT gene complex that causes Crigler-Najjar syndrome type 2.";  
 RL Genomics 18:171-173(1993).  
 RN [9]  
 RP VARIANT CN-I PHE-170 DEL.  
 RX MEDLINE=94043159; PubMed=8226884;  
 RA Ritter J.K., Yeatman M.T., Kaiser C., Gridelli B., Owens I.S.;  
 RT "A phenylalanine codon deletion at the UGT1 gene complex locus of a  
 RT Crigler-Najjar type I patient generates a pH-sensitive bilirubin UDP-  
 RT glucuronosyltransferase.";  
 RL J. Biol. Chem. 268:23573-23579(1993).  
 RN [10]  
 RP VARIANTS CN-I VAL-292; GLU-308; ARG-357; THR-368; ARG-381; PRO-401 AND  
 RP GLU-428.  
 RX MEDLINE=95080780; PubMed=7989045;  
 RA Labrune P., Myara A., Hadchouel M., Ronchi F., Bernard O., Trivin F.,  
 RA Roy Chowdhury N., Roy Chowdhury J., Munnich A., Odievre M.;  
 RT "Genetic heterogeneity of Crigler-Najjar syndrome type I: a study of  
 RT 14 cases.";  
 RL Hum. Genet. 94:693-697(1994).  
 RN [11]  
 RP VARIANTS CN GLU-175; ARG-177; TRP-209; ARG-276 AND PHE-375.  
 RX MEDLINE=95081424; PubMed=7989595;  
 RA Seppen J., Bosma P.J., Goldhoorn B.G., Bakker C.T.M.,  
 RA Roy Chowdhury J., Roy Chowdhury N., Jansen P.L.M.,  
 RA Oude Elferink R.P.J.;  
 RT "Discrimination between Crigler-Najjar type I and II by expression of  
 RT mutant bilirubin uridine diphosphate-glucuronosyltransferase.";  
 RL J. Clin. Invest. 94:2385-2391(1994).  
 RN [12]  
 RP VARIANTS GILBERT SYNDROME ARG-71; GLN-229 AND GLY-367.

RC TISSUE=Liver, and Peripheral blood leukocytes;  
 RX MEDLINE=95231122; PubMed=7715297;  
 RA Aono S., Adachi Y., Uyama E., Yamada Y., Keino H., Nanno T.,  
 RA Koiwai O., Sato H.;  
 RT "Analysis of genes for bilirubin UDP-glucuronosyltransferase in  
 RT Gilbert's syndrome.";  
 RL Lancet 345:958-959(1995).  
 RN [13]  
 RP VARIANTS CN II ARG-71; TRP-209; GLN-229 AND ASP-486.  
 RX MEDLINE=98284535; PubMed=9621515;  
 RA Yamamoto K., Soeda Y., Kamisako T., Hosaka H., Fukano M., Sato H.,  
 RA Fujiyama Y., Dachi Y., Satoh Y., Bamba T.;  
 RT "Analysis of bilirubin uridine 5'-diphosphate (UDP)-  
 RT glucuronosyltransferase gene mutations in seven patients with Crigler-  
 RT Najjar syndrome type II.";  
 RL J. Hum. Genet. 43:111-114(1998).  
 RN [14]  
 RP VARIANT GILBERT SYNDROME ASP-486.  
 RX MEDLINE=98291073; PubMed=9627603;  
 RA Maruo Y., Sato H., Yamano T., Doida Y., Shimada M.;  
 RT "Gilbert syndrome caused by a homozygous missense mutation (Tyr486Asp)  
 RT of bilirubin UDP-glucuronosyltransferase gene.";  
 RL J. Pediatr. 132:1045-1047(1998).  
 CC -!- FUNCTION: UDPGT is of major importance in the conjugation and  
 CC subsequent elimination of potentially toxic xenobiotics and  
 CC endogenous compounds. This isoform glucuronidates bilirubin IX-  
 CC alpha to form both the IX-alpha-C8 and IX-alpha-C12 monoconjugates  
 CC and diconjugate.  
 CC -!- CATALYTIC ACTIVITY: UDP-glucuronate + acceptor = UDP + acceptor  
 CC beta-D-glucuronoside.  
 CC -!- SUBCELLULAR LOCATION: Microsomal.  
 CC -!- ALTERNATIVE PRODUCTS:  
 CC Event=Alternative splicing; Named isoforms=1;  
 CC Comment=A number of isoforms are produced. The different  
 CC isozymes have a different N-terminal domain and a common  
 CC C-terminal domain of 245 residues;  
 CC Name=1;  
 CC IsoId=P22309-1; Sequence=Displayed;  
 CC -!- TISSUE SPECIFICITY: Expressed in liver. Not expressed in skin or  
 CC kidney.  
 CC -!- DISEASE: THE GILBERT'S SYNDROME IS SHOWN TO OCCUR AS A CONSEQUENCE  
 CC OF REDUCED BILIRUBIN TRANSFERASE ACTIVITY. THE DISORDER, IS MOST  
 CC OFTEN DETECTED IN YOUNG ADULTS WITH VAGUE NONSPECIFIC COMPLAINTS.  
 CC A MORE SEVERE INHERITABLE DEFICIENCY IN BILIRUBIN ACTIVITY EXIST  
 CC IN CRIGLER-NAJJAR (CN): PATIENTS WITH TYPE I (RECESSIVE TRAIT)  
 CC HAVE SEVERE HYPERBILIRUBINEMIA AND USUALLY DIE OF KERNICTERUS  
 CC (BILIRUBIN ACCUMULATION IN THE BASAL GANGLIA AND BRAINSTEM NUCLEI)  
 CC WITHIN THE FIRST YEAR OF LIFE. PATIENTS WITH TYPE II (DOMINANT  
 CC TRAIT) HAVE LESS SEVERE HYPERBILIRUBINEMIA AND USUALLY SURVIVE  
 CC INTO ADULTHOOD WITHOUT NEUROLOGIC DAMAGE. PHENOBARBITAL, WHICH  
 CC INDUCES THE PARTIALLY DEFICIENT GLUCURONYL TRANSFERASE, CAN  
 CC DIMINISH THE JAUNDICE.  
 CC -!- SIMILARITY: Belongs to the UDP-glycosyltransferase family.  
 CC -----  
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CC -----

DR EMBL; M84125; AAA61248.1; -.  
DR EMBL; M84124; AAA61247.1; ALT\_SEQ.  
DR EMBL; M84122; AAA61247.1; JOINED.  
DR EMBL; M84123; AAA61247.1; JOINED.  
DR EMBL; M57899; AAA63195.1; -.  
DR EMBL; AF297093; AAG30424.1; -.  
DR EMBL; AC006985; AAF03522.1; -.  
DR EMBL; D87674; BAA25600.1; -.  
DR PIR; A39092; A39092.  
DR Genew; HGNC:12530; UGT1A1.  
DR MIM; 191740; -.  
DR MIM; 143500; -.  
DR MIM; 218800; -.  
DR MIM; 606785; -.  
DR GO; GO:0006789; P:bilirubin conjugation; TAS.  
DR GO; GO:0008210; P:estrogen metabolism; TAS.  
DR InterPro; IPR002213; UDP\_gluco\_trans.  
DR Pfam; PF00201; UDPGT; 1.  
DR PROSITE; PS00375; UDPGT; 1.  
KW Transferase; Glycosyltransferase; Glycoprotein; Transmembrane; Signal;  
KW Multigene family; Microsome; Alternative splicing; Disease mutation.  
FT SIGNAL 1 25 POTENTIAL.  
FT CHAIN 26 533 UDP-GLUCURONOSYLTRANSFERASE 1-1.  
FT TRANSMEM 491 507 POTENTIAL.  
FT CARBOHYD 102 102 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 295 295 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 347 347 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT VARIANT 71 71 G -> R (IN CRIGLER-NAJJAR TYPE II AND  
FT GILBERT SYNDROME).  
FT /FTid=VAR\_009504.  
FT VARIANT 170 170 MISSING (IN CRIGLER-NAJJAR TYPE I; HAS  
FT NEARLY NORMAL ACTIVITY AT PH 7.6 AND IS  
FT INACTIVE AT PH 6.4).  
FT /FTid=VAR\_007695.  
FT VARIANT 175 175 L -> E (IN CRIGLER-NAJJAR TYPE II).

Query Match 24.5%; Score 679; DB 1; Length 533;  
Best Local Similarity 33.8%; Pred. No. 1.1e-45;  
Matches 175; Conservative 93; Mismatches 211; Indels 38; Gaps 13;

Qy 8 LLVGFL--PGVLLSEAAKILTISTVGGSHYLLMDRVSQILQDHGHNVTMLNHNKRGPFMP 65  
|::| || |::| ||| | | ||:| | | | | : :| |  
Db 11 LVLGLLLCVLGPVVS HAGKILLI-PVDGSHWLSMLGAIQQIQRGHEIVVL-----AP 62  
  
Qy 66 D---FKKEEKSYQVISWLAPEDHQRE-FKKSF-----DFFLEETLGGRGKFENLL 111  
| : :: | : :: | || | : || | ||: : : :  
Db 63 DASLYIRDGAFYTLKTY--PVPFQREDVKESFVSLGHNVFENDSFLQRVI---KTYKKIK 117  
  
Qy 112 NVLEYLALQCSHFLNRKDIMDSLKNENFDMVIVETFDYCPFLIAEKLGPFPVAILSTSFG 171  
| ||| | : | : | || : || : : : | | : | : | | | |  
Db 118 KDSAMLLSGCSHLLHNKELMASLAESSFDVMLTDPFLPCSPIVAQYLSLPTVFFLHALPC 177

Qy 172 SLEF---GLPIPLSYVPVFRSLTLDHMDFWGRVKNFLMFFSFCRRQQHMQSTFDNTIKEH 228  
 |||| | | |||| | :|| | |||| |: || : | : |:  
 Db 178 SLEFEATQCPNPFSYVPRPLSSHSDHMTFLQRVKNMLIAFSQNFLCDVVYSPY-ATLASE 236

Qy 229 FTEGSRPVLSHLLLKAEWLFINSDFAFDFARPLLNTVYVGGLMEKPIKVPQDLENFIA 288  
 | : : || | :| || | : ||: || |: ||| : | : | : |  
 Db 237 FLQ-REVTVQDLLSSASVWLFRSDFVKDYPRPIMPNMVFVGGINCLHQNPLSQEFAYIN 295

Qy 289 KFGDSGFVLVTLGSMVNTCQNPEIFKEMNNAFAHLPQGVWKCQCQSHWPKDVHLAANVKI 348  
 | : | | : |||| : : : | : || | : | : : : || | :  
 Db 296 ASGEHGIVVFSLGSMVSEIPEKKAM-AIADALGKIPQTVLWRYTGT---RPSNLANNITL 351

Qy 349 VDWLPQSDLLAHPSIRLFVTHGGQNSIMEAIQHGVPVMVGIPLFQDQPENMVRVEAKKFGV 408  
 | ||||: ||| || | : || | : : | : | |||| : ||||| : | | : | ||  
 Db 352 VKWLPQNDLLGHPMTRAFITHAGSHGVYESICNGVPMVMMPLFGDQMDNAKRMETKGAGV 411

Qy 409 SIQLKKLKAETLALKMKQIMEDKRYKSAAVAASVILRSHPLSPTQRLVGWIDHVLQTGGA 468  
 : : : : | | : | : || || : | : : | : | | : | : : ||  
 Db 412 TLNVLEMTSEDLENALKAVINDKSYKENIMRLSSLHKDRPVEPLDLAVFWVEFVMRHKA 471

Qy 469 THLKPYVFQQPWHEQYLFDFVFLGLTLGLTLWLCGK 505  
 ||: | | : : || ||| : | : : |  
 Db 472 PHLRPAADLTWYQYHSLDVIGFLLAVVLTVAFITFK 508

# RESULT 6

## UDB2\_RAT

ID UDB2\_RAT STANDARD; PRT; 530 AA.  
 AC P08541;  
 DT 01-AUG-1988 (Rel. 08, Created)  
 DT 01-AUG-1988 (Rel. 08, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE UDP-glucuronosyltransferase 2B2 precursor, microsomal (EC 2.4.1.17)  
 DE (UDPGT) (3-hydroxyandrogen specific) (UDPGTR-4) (RLUG23).  
 GN UGT2B2.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Liver;  
 RX MEDLINE=87033594; PubMed=2429951;  
 RA McKenzie P.I.;  
 RT "Rat liver UDP-glucuronosyltransferase. cDNA sequence and expression  
 RT of a form glucuronidating 3-hydroxyandrogens.";  
 RL J. Biol. Chem. 261:14112-14117(1986).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=91369480; PubMed=1909872;  
 RA Haque S.J., Peterson D.D., Nebert D.W., McKenzie P.I.;  
 RT "Isolation, sequence, and developmental expression of rat UGT2B2: the  
 RT gene encoding a constitutive UDP glucuronosyltransferase that  
 RT metabolizes etiocholanolone and androsterone.";  
 RL DNA Cell Biol. 10:515-524(1991).  
 RN [3]  
 RP SEQUENCE OF 30-530 FROM N.A.

RC TISSUE=Liver;  
RX MEDLINE=86120371; PubMed=3003696;  
RA Jackson M.R.; Burchell B.;  
RT "The full length coding sequence of rat liver androsterone UDP-  
RT glucuronyltransferase cDNA and comparison with other members of this  
RT gene family.";  
RL Nucleic Acids Res. 14:779-795(1986).  
CC -!- FUNCTION: UDPGT IS OF MAJOR IMPORTANCE IN THE CONJUGATION AND  
CC SUBSEQUENT ELIMINATION OF POTENTIALLY TOXIC XENOBIOTICS AND  
CC ENDOGENOUS COMPOUNDS. 2B2 ACTS ON VARIOUS ENDOGENOUS STEROIDS,  
CC ESPECIALLY ETIOCHOLANOLONE AND ANDROSTERONE.  
CC -!- CATALYTIC ACTIVITY: UDP-glucuronate + acceptor = UDP + acceptor  
CC beta-D-glucuronoside.  
CC -!- SUBCELLULAR LOCATION: Microsomal.  
CC -!- INDUCTION: Constitutively expressed.  
CC -!- SIMILARITY: Belongs to the UDP-glycosyltransferase family.  
CC -----  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use by non-profit institutions as long as its content is in no way  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
DR EMBL; J02589; AAA42314.1; -.  
DR EMBL; M74439; -; NOT\_ANNOTATED\_CDS.  
DR EMBL; X03478; CAA27198.1; -.  
DR PIR; A40467; A40467.  
DR InterPro; IPR002213; UDP\_gluco\_trans.  
DR Pfam; PF00201; UDPGT; 1.  
DR PROSITE; PS00375; UDPGT; 1.  
KW Transferase; Glycosyltransferase; Glycoprotein; Transmembrane; Signal;  
KW Multigene family; Microsome.  
FT SIGNAL 1 23 BY SIMILARITY.  
FT CHAIN 24 530 UDP-GLUCURONOSYLTRANSFERASE 2B2.  
FT TRANSMEM 494 510 POTENTIAL.  
FT CARBOHYD 316 316 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CONFLICT 159 159 D -> E (IN REF. 3).  
FT CONFLICT 286 286 A -> S (IN REF. 3).  
FT CONFLICT 351 351 N -> I (IN REF. 3).  
FT CONFLICT 363 363 L -> I (IN REF. 3).  
SQ SEQUENCE 530 AA; 60985MW; F2FFF3E23E2D75B2 CRC64;

Query Match 24.5%; Score 677.5; DB 1; Length 530;  
Best Local Similarity 33.5%; Pred. No. 1.4e-45;  
Matches 170; Conservative 87; Mismatches 218; Indels 33; Gaps 13;

Qy 34 SHYLLMDRVSQILQDHGHNVTMLNHKRGPFMPDFKKEEKSYQVISW-LAPEDHQREFKKS 92  
||::: : | ||||: | : :: | :::: | ||  
Db 34 SHWMNIKIILDELVQRGHEVTVLKPSAYFFLDPKKSSDLKFEIFSTSISKDELQNHFIKL 93  
Qy 93 FDFFLLEE-----TLGGRGKFENLLNVLEYLALQ-CSHFLNRKDIMDSLKNENFDMVIVET 146  
| : | | :||: | | | :| :| | : ||:: :  
Db 94 LDVWTYELPRDTCLSYSPILQNLVYEFSYFYLSICKDAVSNKQLMTKLQESKFDVLFADP 153  
Qy 147 FDYCPFLIAEKLKGPVAILSTSFG-SLEFGLP---IPLSYVPVFRSLTDMDFWGRVK 202

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      | | | | | | : | | | | | : | | | | | | | | | |
Db    154 VASCGDLIAELLHIPFLYSLSFSPGHKLEKSIGKFILPPSYVPVILSGLAGKMTFIDRVK 213

QY    203 NF--LMFFSF-CRRQQHMQ-STFDNTIKEHFTEGSRPVLSHLLLKAEWFINSDFAFDFA 258
      | : : | | | : | : | | : | | : | : | | : |
Db    214 NMICMLYFDFWFERLRHKEWDTFYSEIL-----GRPTTVDETMASKVEIWLIRSYWDLKFP 268

QY    259 RPLLENTVYVGGLMKEPIKPVPQDLENFIAKFGDSGFVLVTLGSMVNTCQNPFIKEMNN 318
      | | | | | : | | | | | : | : | : | : | : | : | : |
Db    269 HPTLPNVDIYIGGLHCKPAKPLPKDMEEFVQSSGEHGVVVFSLGSMVS-----NMTEEKAN 323

QY    319 ----AFAHLPOGVWKQCQSHWPKDVHLAANVKIVDWLPQSDLLAHPsirLFVTHGGQNS 374
      | | : | | | : | | | | | | | | : | | | | | |
Db    324 AIAWALAQIPQKVLWKFD---GKTPATLGPNTRVYKWLQNDLLGHPKTKAFVTHGGANG 380

QY    375 IMEAIQHGVMVGIPPLFGDQPENMVRVEAKKFGVSIQLKKLKAETLALKMKQIMEDKRYK 434
      : | | | | : | | | | | | | | : | | | | : : : : : : |
Db    381 LYEAIIYHGIPMIGIPLFGDQPDNIAHMAVAKGAASLNIRTMSKLDFLSALEEVIDNPFYK 440

QY    435 SAAVAASVILRSHPLSPTQRLVGWIDHVLQTGGATHLKPYVFQQPWHEQYLFDFVFVLLG 494
      : | | | | : | | | | | | | : : : | | | | | : : : | | |
Db    441 KNVMLLSTIHHDQPMKPLDRAVFWIEFIMRHKGAKHLRPLGHNLPWYQYHSLDVIGFLLT 500

QY    495 LTLGTLWLWLCGK-LLGMAVWWLRGARKVK 521
      | | | | | : : : : | : |
Db    501 CFAVIAALTVMKCLLEMYRFFVKKEKKMK 528

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# RESULT 7

## UDBK\_MACFA

```

ID    UDBK_MACFA      STANDARD;      PRT;    530 AA.
AC    077649;
DT    15-DEC-1998 (Rel. 37, Created)
DT    15-DEC-1998 (Rel. 37, Last sequence update)
DT    28-FEB-2003 (Rel. 41, Last annotation update)
DE    UDP-glucuronosyltransferase 2B20 precursor, microsomal (EC 2.4.1.17)
DE    (UDPGT).
GN    UGT2B20.
OS    Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC    Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC    Cercopithecinae; Macaca.
OX    NCBI_TaxID=9541;
RN    [1]
RP    SEQUENCE FROM N.A., AND CHARACTERIZATION.
RC    TISSUE=Liver, and Prostate;
RX    MEDLINE=99112924; PubMed=9895303;
RA    Barbier O., Belanger A., Hum D.W.;
RT    "Cloning and characterization of a simian UDP-glucuronosyltransferase
RT    enzyme UGT2B20, a novel C19 steroid-conjugating protein.";
RL    Biochem. J. 337:567-574(1999).
CC    -!- FUNCTION: UDPGTs are of major importance in the conjugation and
CC    subsequent elimination of potentially toxic xenobiotics and
CC    endogenous compounds. This isozyme has glucuronidating capacity
CC    with androgens, such as testosterone, dihydrotestosterone (DHT)
CC    and 3alpha-Diol. It is also active on catecholoeestrogens including
CC    1,3,5,10-oestratriene-3, 4-diol-17-one.

```

```
CC      -!- CATALYTIC ACTIVITY: UDP-glucuronate + acceptor = UDP + acceptor
CC          beta-D-glucuronoside.
CC      -!- SUBCELLULAR LOCATION: Microsomal.
CC      -!- SIMILARITY: Belongs to the UDP-glycosyltransferase family.
CC      -----
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
CC      between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC      the European Bioinformatics Institute. There are no restrictions on its
CC      use by non-profit institutions as long as its content is in no way
CC      modified and this statement is not removed. Usage by and for commercial
CC      entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC      or send an email to license@isb-sib.ch).
CC      -----
DR      EMBL; AF072223; AAD08808.1; -.
DR      InterPro; IPR002213; UDP_gluco_trans.
DR      Pfam; PF00201; UDPGT; 1.
DR      PROSITE; PS00375; UDPGT; 1.
KW      Transferase; Glycosyltransferase; Glycoprotein; Transmembrane; Signal;
KW      Multigene family; Microsome.
FT      SIGNAL          1          23          POTENTIAL.
FT      CHAIN           24         530         UDP-GLUCURONOSYLTRANSFERASE 2B20.
FT      TRANSMEM        495         515         POTENTIAL.
FT      CARBOHYD         65          65         N-LINKED (GLCNAC. . .) (POTENTIAL).
FT      CARBOHYD        103         103         N-LINKED (GLCNAC. . .) (POTENTIAL).
FT      CARBOHYD        316         316         N-LINKED (GLCNAC. . .) (POTENTIAL).
FT      CARBOHYD        483         483         N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ      SEQUENCE       530 AA;  61225 MW;  A5EB47F8D517D8DA CRC64;
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Qy	34	SHYLLMDRVSQILQDHGHNVMTLNNHKGPFMPDFKKKEESYQVI-SWLAPEDHQREFFKS	92
Db	34	SHWINMKTILEELVRRRHEVTVLTSASTFVNDSKSSAIKFEVYPTSLTKNDMEDSLMKL	93
Qy	93	FDFFLLEETLGGRGKFENLLNVLEYLALQ-----CSHFLNRKDIMDSLKNENFDMVIV	144
Db	94	LDIWTYSI--SNSTFLSYFSKLQELCWEYYYYSEKLCKDAVLNKKLMTKLIKETKFDVILA	151
Qy	145	ETFDYCPFLIAEKLGKPFVAILSTSFG-SLE---FGLPIPLSYVPVFRSLLTDHMDFWGR	200
Db	152	DALNPCGELLAELFNIPFVYSLRFTVGYTFEKNGGGFLFPPSYVPVVMSELSDQMTFTER	211
Qy	201	VKNFL--MFFSFCCRQOHMQSTFDNTIKEHFTEGSRPVLSHLLLKAELWFINSDFAFDFA	258
Db	212	IKNMIHKLYFDFW-FQIHDIKKWDQFYSE--VLGRPTTLFETMRKAEMWLIRTYWDFEFP	268
Qy	259	RPLLNPNTVYVGGLMKPIKVPVQDLNFIAKFGDSGFVLVTLGSMVNTCQNPEIFKEMNN	318
Db	269	RPFLPNVDFVGGHLHCKPAKPLPKEMEEFVQSSGENGVVVFSLGSMISN-MSEERANMIAS	327
Qy	319	AFAHLPQGVIWKQCQSHWPKDVHLAANVKIVDWLPQSDLLAHPSIRLFVTHGGQNSIMEA	378
Db	328	ALAQIPQKVLWKFD---GKKPNTLGSNTRLYKWLPQNDLLGHPKTKAFITHGGTNGIYEA	384
Qy	379	IOHGVPVMGVIPLFGDOPENMVRVEAKKFGVSIQLKKLKAETLALKMKQIMEDKRYKSAAV	438



```

      | ||:||||||| || :|:| :: |   :|: :: : : |   :| :: : || |:
Db      385 IYHGIPMVGIPLFADQHDNIVHMKVGAALSVDIRTMSSRDLLNALKSVINEPIYKENAM 444

Qy      439 AASVILRSHPLSPTQRLVGWIDHVLQTGGATHLKPYVFQQPWHEQYLFDFVFLGLGLTLG 498
      | |   |: | | | ||: |: | | ||:   | : : || |||
Db      445 KLSRIHHDQPMKPLDRAVFWIEFVMRHKGAKHLRVAAHNLTWQYHSLDVIAFLACVAA 504

Qy      499 TLWLCGK 505
      ::: |
Db      505 VIFIITK 511

```

RESULT 8

UDBD\_RABIT

```

ID      UDBD_RABIT      STANDARD;      PRT;      531 AA.
AC      P36512;
DT      01-JUN-1994 (Rel. 29, Created)
DT      01-JUN-1994 (Rel. 29, Last sequence update)
DT      16-OCT-2001 (Rel. 40, Last annotation update)
DE      UDP-glucuronosyltransferase 2B13 precursor, microsomal (EC 2.4.1.17)
DE      (UDPGT) (EGT10).
GN      UGT2B13.
OS      Oryctolagus cuniculus (Rabbit).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX      NCBI_TaxID=9986;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=New Zealand white; TISSUE=Liver;
RX      MEDLINE=93315511; PubMed=8325897;
RA      Tukey R.H., Pendurthi U.R., Nguyen N.T., Green M.D., Tephly T.R.;
RT      "Cloning and characterization of rabbit liver UDP-
RT      glucuronosyltransferase cDNAs. Developmental and inducible expression
RT      of 4-hydroxybiphenyl UGT2B13.";
RL      J. Biol. Chem. 268:15260-15266(1993).
CC      -!- FUNCTION: UDPGT IS OF MAJOR IMPORTANCE IN THE CONJUGATION AND
CC      SUBSEQUENT ELIMINATION OF POTENTIALLY TOXIC XENOBIOTICS AND
CC      ENDOGENOUS COMPOUNDS. ACTS ON SMALL PHENOLIC AGENTS SUCH AS 2-
CC      NAPHTOL AND 4-METHYLBELLIFERONE AS WELL AS BULKY PHENOLIC
CC      COMPOUNDS LIKE 2-HYDROXY- AND 4-HYDROXYBIPHENYL. IN CONTRAST TO
CC      2B16 IT IS ACTIVE TOWARD OCTYLGALLATE.
CC      -!- CATALYTIC ACTIVITY: UDP-glucuronate + acceptor = UDP + acceptor
CC      beta-D-glucuronoside.
CC      -!- SUBCELLULAR LOCATION: Microsomal.
CC      -!- DEVELOPMENTAL STAGE: Expressed primarily in adult rabbits.
CC      -!- SIMILARITY: Belongs to the UDP-glycosyltransferase family.
CC      -----
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
CC      between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC      the European Bioinformatics Institute. There are no restrictions on its
CC      use by non-profit institutions as long as its content is in no way
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CC      entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC      or send an email to license@isb-sib.ch).
CC      -----
DR      EMBL; L01081; AAA18020.1; -.
DR      PIR; B47113; B47113.

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DR InterPro; IPR002213; UDP\_gluco\_trans.  
 DR Pfam; PF00201; UDPGT; 1.  
 DR PROSITE; PS00375; UDPGT; 1.  
 KW Transferase; Glycosyltransferase; Glycoprotein; Transmembrane; Signal;  
 KW Multigene family; Microsome.  
 FT SIGNAL 1 24  
 FT CHAIN 25 531 UDP-GLUCURONOSYLTRANSFERASE 2B13.  
 FT TRANSMEM 495 511 POTENTIAL.  
 FT CARBOHYD 69 69 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 101 101 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 317 317 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SQ SEQUENCE 531 AA; 60552 MW; 961DA58AC4CB9932 CRC64;

Query Match 24.2%; Score 670; DB 1; Length 531;  
 .Best Local Similarity 32.6%; Pred. No. 5.4e-45;  
 Matches 169; Conservative 90; Mismatches 206; Indels 54; Gaps 14;

Qy 34 SHYLLMDRVSQILQDHGHNVMTL-----NHKRG----PFMPDFKKEEKSYQVISW 79  
 ||:: | : | || ||:| |:: | | ::::| : |  
 Db 35 SHWMNMKTILDALVQQGHEVTVLRSSASIVIGSNNESGIKFETFHTSYRKDEIENFFMDW 94  
 Qy 80 LAPEDHQREFKKSFDFFLE---ETLGGRGKFENLLNVLEYLAL---QCSHFLNRKDIMDS 133  
 :| :: :| || :::| : | : | :|  
 Db 95 F-----YKMIYNVSIESYWETFS-----LTKMVILKYSDICEDICKEVILNKKLMTK 141  
 Qy 134 LKNENFDMVIVETFDYCPFLIAEKLKGP-----FVAILSTSFGSLEFGLPIPLSYVPV 186  
 |: ||:: : |::| | | || : | | |||  
 Db 142 LQESRFDVVLADPVSPGGELLAELLKIPLVYSLRGFVGYMLQKHGG---GLLLPPSYVPV 198  
 Qy 187 FRSLTLDHMDFWGRVKNFL--MFFSFCRRQQHMQSTFDNTIKEHFTEGSRPV--LSHLLLK 243  
 | | | ||:| | :| | : : :| | || | :|  
 Db 199 MMSGGLGSQMTFMERVQNLLCVLYFDFW--FPKFNEKRWDQFYSEVL---GRPVTFLELMGK 254  
 Qy 244 AELWFINSDFAFDFARPLLENTVYVGGLMEKPIKPVPQDLENFIAKFGDSGFVLVTLGSM 303  
 |::| | | : :| ||||| :||| || ||:|::|:|: | : | | :|||  
 Db 255 ADMWLIRSYWDLEFPRPLLPNFDFIGGLHCKPAKPLPQEMEDFVQSSGEEGVVVFSLGSM 314  
 Qy 304 VNTCQNPEIFKEMNNAFAHLPQGVWKQCQSHWPKDVHLAANVKIVDWLPQSDLLAHPST 363  
 :: | : :| | || |:: : | | :| :: |::| || ||  
 Db 315 ISNL-TEERANVIASALAQLPQKVLWRFE---GKKPDMLGSNTRLYKWIPQNDLLGHPKT 370  
 Qy 364 RLFVTHGGQNSIMEAIQHGVPVGIPLFGDQPENMVRVEAKKFGVSIQLKKLKAETLALK 423  
 : |::||| | : || |::|||:||||| :|:| ::|| | : || : : |  
 Db 371 KAFITHGGANGVFEAIYHGIPMVGLPLFGDQLDNIVYMKAKGAAVKLNLTMTSSADLLNA 430  
 Qy 424 MKQIMEDKRYKSAAVAASVILRSHPLSPTQRLVGWIDHVLQTGGATHLKPYVFQQPWHEQ 483  
 :| :: | || | : | | | : | | ||::|:| || ||: |::  
 Db 431 LKTVINDPSYKENAMTSLRIHHDQPMKPLDRAVFWIEYVMRHKGAKHLRVAHDLTWYQY 490  
 Qy 484 YLFDVVFVLLGLTLGLTLWLCGKLLGMAVWWLRGARKVKE 522  
 : || || | : | | : : || | :  
 Db 491 HSLDVIGFLLACVAITTYLIVKCCILVYRYVLGAGKKKK 529

RESULT 9  
 UD11\_MOUSE  
 ID UD11\_MOUSE STANDARD; PRT; 535 AA.

AC Q63886;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE UDP-glucuronosyltransferase 1-1 precursor, microsomal (EC 2.4.1.17)  
 DE (UDPGT) (UGT1\*1) (UGT1-01) (UGT1.1) (UGT1A1) (UGTBR1).  
 GN UGT1A1 OR UGT1.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=93219265; PubMed=8464825;  
 RA Kong A.N., Ma M., Tao D., Yang L.;  
 RT "Molecular cloning of two cDNAs encoding the mouse bilirubin/phenol  
 RT family of UDP-glucuronosyltransferases (mUGTBr/p).";  
 RL Pharm. Res. 10:461-465(1993).  
 CC -!- FUNCTION: UDPGT is of major importance in the conjugation and  
 CC subsequent elimination of potentially toxic xenobiotics and  
 CC endogenous compounds.  
 CC -!- CATALYTIC ACTIVITY: UDP-glucuronate + acceptor = UDP + acceptor  
 CC beta-D-glucuronoside.  
 CC -!- SUBCELLULAR LOCATION: Microsomal.  
 CC -!- ALTERNATIVE PRODUCTS:  
 CC Event=Alternative splicing; Named isoforms=1;  
 CC Comment=A number of isoforms are produced. The different  
 CC isozymes have a different N-terminal domain and a common  
 CC C-terminal domain of 245 residues;  
 CC Name=1;  
 CC IsoId=Q63886-1; Sequence=Displayed;  
 CC -!- INDUCTION: By dioxin.  
 CC -!- SIMILARITY: Belongs to the UDP-glycosyltransferase family.  
 CC -----  
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 CC -----  
 DR EMBL; S64760; AAB26033.2; -.  
 DR MGD; MGI:98898; Ugt1a1.  
 DR InterPro; IPR002213; UDP\_gluco\_trans.  
 DR Pfam; PF00201; UDPGT; 1.  
 DR PROSITE; PS00375; UDPGT; 1.  
 KW Transferase; Glycosyltransferase; Glycoprotein; Transmembrane; Signal;  
 KW Multigene family; Microsome; Alternative splicing.  
 FT SIGNAL 1 29 POTENTIAL.  
 FT CHAIN 30 535 UDP-GLUCURONOSYLTRANSFERASE 1-1.  
 FT TRANSMEM 493 509 POTENTIAL.  
 FT CARBOHYD 89 89 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 297 297 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 435 435 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SQ SEQUENCE 535 AA; 60123 MW; B5AE3C209979BBB8 CRC64;

Query Match 24.2%; Score 669; DB 1; Length 535;  
 Best Local Similarity 31.7%; Pred. No. 6.6e-45;  
 Matches 174; Conservative 101; Mismatches 216; Indels 58; Gaps 15;

```

      5 RVLVLVGFLLP---GVLLSEAAKILTISTVGGSHYLLMDRVSQILQDHGHNVTMLNHKRG 61
      |::||: :|| | | :| : : ||:| | | | | | | :|
      9 RLLLLLPYLLLCVFGPYASHAGRL--VFPMDGSHWLSMLGVIQQLQKKGHEVVVI----A 63

Qy      62 PFMPDFKKEEKSYQVISWLAPEDHQREFKKSFDFFLEETLGGRGKFEN---LLNVLE-YL 117
      | | | | : : | | :| : | | | | | | | :| :|
Db      64 PEASIHKEGSFYTLRKFVPFQ-----KENVTATIVEL--GRTAFNQDSFLLRVVKIYM 116

Qy      118 ALQ-----CSHFLNRKDIMDSLKNENFDMVIVETFDYCPFLIAEKLKGP---FVAI 165
      :: | | | : : | | :| :| : : | | :| :| | | :|
Db      117 KVKRDSMLLAGCSHLLHNAEFMASLEESHFDALLTDPFLPCGSIVAQYLTVPTVYFLNK 176

Qy      166 LSTSFSGSLEFGLPIPLSYVPVFRSLTDMDFWGRVKNFLMFFS---FCRRQQHMQSTFD 222
      | | | | :| | | | | | :| | :| | | | :| | | :|
Db      177 LPCSLDSEATQCPVPLSYVPKSLSENSDRMFLQRVKNVLLAVSENFCRVVYSPYGLSLA 236

Qy      223 NTIKEHFTGSRPVLSHLLKAEWLFINSDFAFDARPLLNTVYVGLMEKPIKVPVQD 282
      | : : | | :| : | | | :| | :| | | :| :| :| :| :| :|
Db      237 TEILQ-----KEVTQDLLSPASIWLMSRDFVKDYPRPIMPNMVFIGGINCLQKKPLSQE 291

Qy      283 LENFIAKFGDSGFVLVTLGSMVNTCQNPEIFKEMNNAFAHLPGGVWKCQCASHWPKDVHL 342
      | :: | : | | :| | | :| :| :| :| :| :| :| :| :|
Db      292 FEAYVNASGEHGIVVFSLGSMVSEIPEKKAM-EIAEALGRIPQTVLWRYTGT---RPSNL 347

Qy      343 AANVKIVDWLPQSDLLAHPISIRLFVTHGGQNSIMEAIQHGVPVMGIPLEFGDQPENMVRVE 402
      | | :| | | :| :| | | :| | | :| | | :| | | :| | | :|
Db      348 AKNTILVKWLQNDLIGHPKTRAFITHSGSHGIYEGICNGVPMVMPLFGDQMDNAKRME 407

Qy      403 AKKFGVSIQLKKLKAETLALKMKQIMEDKRYKSAAVAASVILRSHPLSPTQRLVGWIDHV 462
      : | : : : :| :| :| :| :| :| :| :| :| :| :| :| :|
Db      408 TRGAGVTINVLEMTADDLENALKTVINNKSYKENIMRLSSLHKDRPIEPLDLAVFEVVEYV 467

Qy      463 LQTGGATHLKPYVVFQQPWHEQYLFDFVFLGLTLGLTLWL-----CGKLLGMAVWWL 514
      :: | | | :| :| :| | | :| :| :| :| :| :| :| :|
Db      468 MRHKGAPHLRPAADLTWYQYHSLDVIGFLLAIVLTVVVFVFKCCAYGCRKCFG----- 521

Qy      515 RGARKVKET 523
      | :| :| :|
Db      522 -GKGRVKKS 529
  
```

RESULT 10

UDB1\_RAT

ID UDB1\_RAT STANDARD; PRT; 529 AA.

AC P09875;

DT 01-MAR-1989 (Rel. 10, Created)

DT 01-MAR-1989 (Rel. 10, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE UDP-glucuronosyltransferase 2B1 precursor, microsomal (EC 2.4.1.17)

DE (UDPGT) (UDPGTR-2).

GN UGT2B1.

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Liver;  
 RX MEDLINE=86196018; PubMed=3084479;  
 RA McKenzie P.I.;  
 RT "Rat liver UDP-glucuronosyltransferase. Sequence and expression of a  
 RT cDNA encoding a phenobarbital-inducible form.";  
 RL J. Biol. Chem. 261:6119-6125(1986).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=90293083; PubMed=2113533;  
 RA McKenzie P.I., Rodbourn L.;  
 RT "Organization of the rat UDP-glucuronosyltransferase, UDPGTr-2, gene  
 RT and characterization of its promoter.";  
 RL J. Biol. Chem. 265:11328-11332(1990).  
 CC -!- FUNCTION: UDPGT is of major importance in the conjugation and  
 CC subsequent elimination of potentially toxic xenobiotics and  
 CC endogenous compounds.  
 CC -!- CATALYTIC ACTIVITY: UDP-glucuronate + acceptor = UDP + acceptor  
 CC beta-D-glucuronoside.  
 CC -!- SUBCELLULAR LOCATION: Microsomal.  
 CC -!- INDUCTION: By phenobarbital.  
 CC -!- SIMILARITY: Belongs to the UDP-glycosyltransferase family.  
 CC -----  
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 CC -----  
 DR EMBL; M13506; AAA42313.1; -.  
 DR EMBL; M35086; AAA42310.1; -.  
 DR EMBL; M35202; AAA42310.1; JOINED.  
 DR EMBL; M35080; AAA42310.1; JOINED.  
 DR EMBL; M35082; AAA42310.1; JOINED.  
 DR EMBL; M35083; AAA42310.1; JOINED.  
 DR PIR; A42233; A42233.  
 DR InterPro; IPR002213; UDP\_gluco\_trans.  
 DR Pfam; PF00201; UDPGT; 1.  
 DR PROSITE; PS00375; UDPGT; 1.  
 KW Transferase; Glycosyltransferase; Glycoprotein; Transmembrane; Signal;  
 KW Multigene family; Microsome.  
 FT SIGNAL 1 23 BY SIMILARITY.  
 FT CHAIN 24 529 UDP-GLUCURONOSYLTRANSFERASE 2B1.  
 FT TRANSMEM 494 510 POTENTIAL.  
 FT CARBOHYD 134 134 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 316 316 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SQ SEQUENCE 529 AA; 60484 MW; 14DF0224BF1C3044 CRC64;

Query Match 24.1%; Score 668; DB 1; Length 529;  
 Best Local Similarity 32.2%; Pred. No. 7.8e-45;  
 Matches 175; Conservative 89; Mismatches 229; Indels 50; Gaps 15;

Qy 6 VLLLVGFLLPGLVLLSEAAKILTISTVGGSHYLLMDRVSQILQDHGHNVTMLNHKRGPFMP 65  
 Db 11 LIQLICYFRPGA----CGKVLVWPT-EYSHWINIKIILNELAQRGHEVTVLVSSASILIE 65

Qy 66 DFKKEEKSYQVISW-LAPEDHQREFKKSDFDFLE--ETLG---GRGKFENLLN---VLE 115  
 Db 66 PTKESSINFETIYSVPLSKSDLEYSFAKWIDEWTRDFETLSIWTTYYSKMVKVFNEYSADVVE 125

Qy 116 YLALQCSHFLNRKDIMDSLKNENFDMVIVETFDYCPFLIAEKLKGPVFAILSTSFG---- 171  
 Db 126 NL---CKALIWNKSLMKKLQGSQFDVILADAVGPCGELLAELLKTPLVYSLRFCPGYRCE 182

Qy 172 SLEFGLPIPLSYVPVFRSLTLDHMDFWGRVKNFL--MFFSFCRRQQHMQSTFDNTIKEHF 229  
 Db 183 KFSGGLPLPPSYVPVVLSELSDRMTFVERVKNMLQMLYFDF-----WFQPFKEKSWSQFY 237

Qy 230 TE--GSRPVLSHLLLKAEWLFINSDFAFDFARPLLNTVYVGGIMEKPIKPVPQDLENFI 287  
 Db 238 SDVLGRPTTLTEMMGKADIWLIRTFWDLEFPHPLPNFDFVGGHCKPAKPLPREMEEFV 297

Qy 288 AKFGDSGFVLVTLGSMVNTCQNPEIFKEMNNAFAHLPPQGVWKCQCSHWPKDVHLAANVK 347  
 Db 298 QSSGEHGVVVSFLGSMVKNL-TEEKANVVASALAQIPQKVWVRFD---GKKPDTLGSNTR 353

Qy 348 IVDWLPQSDLLAHPISIRLFVTHGGQNSIMEAIQHGVPMVGIPLEFGDQPENMVRVEAKKFG 407  
 Db 354 LYKWIPQNDLLGHPKTKAFVAHGGTNGIYEAIYHGIPIVGIPLEFADQPDNINHMVAKGAA 413

Qy 408 VSIQLKKLKAETLALKMKQIMEDKRYKSAAVAASVILRSHPLSPTQRLVGVWIDHVLQTGG 467  
 Db 414 VRVDFSILSTTGLLTALKIVMNDPSYKENAMRLSRIHHDQPVKPLDRAVFWIEYVMRHKG 473

Qy 468 ATHLKPYVFQQPWHEQYLFDFVFLGLTLGT-----LWLCGKLLGMAVWWLRGARK 519  
 Db 474 AKHLRSTLHDLWSFQYHSLDVIGFLLLCVGVVFIITKFCCLFCCRKTANM-----GKK 526

Qy 520 VKE 522  
 Db 527 KKE 529

# RESULT 11

UD15\_RAT

ID UD15\_RAT STANDARD; PRT; 531 AA.

AC Q64638;

DT 01-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE UDP-glucuronosyltransferase 1-5 precursor, microsomal (EC 2.4.1.17)

DE (UDPGT) (UGT1\*5) (UGT1-05) (UGT1.5) (UGT1A5) (B5).

GN UGT1.

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

OX NCBI\_TaxID=10116;

RN [1]

RP SEQUENCE OF 1-286 FROM N.A.

RC STRAIN=Wistar;  
 RX MEDLINE=95332265; PubMed=7608130;  
 RA Emi Y., Ikushiro S.I., Iyanagi T.;  
 RT "Drug-responsive and tissue-specific alternative expression of  
 RT multiple first exons in rat UDP-glucuronosyltransferase family 1  
 RT (UGT1) gene complex.";  
 RL J. Biochem. 117:392-399(1995).  
 RN [2]  
 RP SEQUENCE OF 287-531 FROM N.A.  
 RC TISSUE=Liver;  
 RX MEDLINE=90274676; PubMed=2112380;  
 RA Sato H., Koiwai O., Tanabe K., Kashiwamata S.;  
 RT "Isolation and sequencing of rat liver bilirubin UDP-  
 RT glucuronosyltransferase cDNA: possible alternate splicing of a common  
 RT primary transcript.";  
 RL Biochem. Biophys. Res. Commun. 169:260-264(1990).  
 CC -!- FUNCTION: UDPGT is of major importance in the conjugation and  
 CC subsequent elimination of potentially toxic xenobiotics and  
 CC endogenous compounds.  
 CC -!- CATALYTIC ACTIVITY: UDP-glucuronate + acceptor = UDP + acceptor  
 CC beta-D-glucuronoside.  
 CC -!- SUBCELLULAR LOCATION: Microsomal.  
 CC -!- ALTERNATIVE PRODUCTS:  
 CC Event=Alternative splicing; Named isoforms=1;  
 CC Comment=A number of isoforms may be produced. Isoforms have a  
 CC different N-terminal domain and a common C-terminal domain of  
 CC 245 residues;  
 CC Name=1;  
 CC IsoId=Q64638-1; Sequence=Displayed;  
 CC -!- SIMILARITY: Belongs to the UDP-glycosyltransferase family.  
 CC -----  
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 CC -----  
 DR EMBL; D38069; BAA07263.1; -.  
 DR EMBL; M34007; AAA42312.1; ALT\_TERM.  
 DR InterPro; IPR002213; UDP\_gluco\_trans.  
 DR Pfam; PF00201; UDPGT; 1.  
 DR PROSITE; PS00375; UDPGT; 1.  
 KW Transferase; Glycosyltransferase; Glycoprotein; Transmembrane; Signal;  
 KW Multigene family; Microsome; Alternative splicing.  
 FT SIGNAL 1 25 POTENTIAL.  
 FT CHAIN 26 531 UDP-GLUCURONOSYLTRANSFERASE 1-5.  
 FT TRANSMEM 489 505 POTENTIAL.  
 FT CARBOHYD 116 116 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 131 131 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 139 139 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 293 293 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 431 431 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SQ SEQUENCE 531 AA; 59993 MW; 04148C1BA6CAAC80 CRC64;

Query Match

24.0%; Score 665; DB 1; Length 531;

Best Local Similarity 30.5%; Pred. No. 1.3e-44;  
Matches 169; Conservative 102; Mismatches 216; Indels 68; Gaps 15;

```

Qy      1 MAGQRVLLLVGFLLPGVLLSEAAKILTISTVGGSHYLLMDRVSQILQDHGHNVMTLNHHR 60
      : |   ||| : : |   : | : | : : ||| : | | : |   ||   : |
Db      7 LQGLAGLLLLLYALP---WAEKGKVL-VFPMEGSHWLSMRDVVRELHARGHQAVVL---- 58

Qy     61 GPFMPDFKKEEKSYQVISWLAPEDHQ-----REFKKSFD-----FFLEETLGGRGKF 107
      | :   ||| : : : : |   |   |   | :   ||| :
Db     59 APEVTVHIKEEDFFTLLQTYPPVYTRQGFRQQMMRNIVVFETGNYVKTFLETS----- 111

Qy    108 ENLLNVLEYLALQCSHFLNRKDIMDSLKNENFDMVIVETFDYCPFLIAEKLKGP---FVA 164
      | | | : |   | : | : : : | : ||| : :   | : | : | | | :
Db    112 EILKNISTVLLRSCMNLLHNGSLLQHLNSSSFDMVLTDPVIPCGQVLAKYLGIPTVFFLR 171

Qy    165 ILSTSFGSLEFGLPIPLSYVPVFRSLLTDHMDFWGRVKN-----FLMFFSFCRRQQH 216
      :   |   | | ||| : : | : ||| |   |||   : : | | | :
Db    172 YIPCGIDSEATQCPKPSSYIPNLLTMLSDHMTFLQRVKNMLYPLALKYICHFSFTRYESL 231

Qy    217 MQSTFDNTIKEHFTEGSRPVLSHLLLLKAELWFINSDFAFDFARPLLNTVYVGGGLMEKPI 276
      :   |   ||| |   | : |   || ||| : || : || | : : || :
Db    232 ASELLQREVS--LVE---VLSH---ASVWLFRGDFVFDYPRPVMNPMVFIGGINCVIK 281

Qy    277 KPVPQDLENFIAKFGDSGFVLVTLGSMVNTCQNPEIFKEMNNAFAHLPQGVWKCQCQSHW 336
      || : | : : | : | | : : ||| : :   | : |   : || : : : :
Db    282 KPLSQEFEAYVNASGEHGIVVFSLGSMVSEIPEKKAM-EIAEALGRIPQTLWRYTGT-- 338

Qy    337 PKDVHLAANVKIVDWLPQSDLLAHPSIRLFVTHGGQNSIMEAIQHGVPMVGIPFLFGDQPE 396
      :   : || |   : | ||| : || | | | : | | | : ||| | : ||| | :
Db    339 -RPSNLAKNTILVKWLPQNDLLGHPKARAFITHSGSHGIYEGICNGVPMVMMPFLFGDQMD 397

Qy    397 NMVRVEAKKFGVSIQLKKLKAETLALKMKQIMEDKRYKSAAVAASVILRSHPLSPTQRLV 456
      | | : | : || : : : : | : |   : | : : | ||   : | : : | : | |
Db    398 NAKRMETRGAGVTNLNVLEMTADDLENALKTVINNKSYKENIMRLSSLHKDRPIEPLDLAV 457

Qy    457 GWIDHVLQTGGATHLKPYPVFQPPWHEQYLFDFVFVFLGLTLGLTLWL-----CGKLLG 508
      | : : | : : || ||| : | : : : || ||| : | : : :   | | |
Db    458 FWVEYVMRHKGAPHLRPAAHDLTWYQYHSLDVIGFLLAIVLTVVFIVYKSCAYGCRKCFG 517

Qy    509 MAVWWLRGARKVKET 523
      |   : || : :
Db    518 -----GKGRVKKS 525

```

# RESULT 12

UDBJ\_MACFA

ID UDBJ\_MACFA STANDARD; PRT; 528 AA.

AC Q9XT55;

DT 30-MAY-2000 (Rel. 39, Created)

DT 30-MAY-2000 (Rel. 39, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE UDP-glucuronosyltransferase 2B19 precursor, microsomal (EC 2.4.1.17).

GN UGT2B19.

OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;

OC Cercopithecinae; Macaca.



OX NCBI\_TaxID=9541;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Liver, and Prostate;  
 RX MEDLINE=99203465; PubMed=10102998;  
 RA Belanger G., Barbier O., Hum D.W., Belanger A.;  
 RT "Molecular cloning, expression and characterization of a monkey  
 RT steroid UDP-glucuronosyltransferase, UGT2B19, that conjugates  
 RT testosterone.";  
 RL Eur. J. Biochem. 260:701-708(1999).  
 CC -!- FUNCTION: UDPGT IS OF MAJOR IMPORTANCE IN THE CONJUGATION AND  
 CC SUBSEQUENT ELIMINATION OF POTENTIALLY TOXIC XENOBIOTICS AND  
 CC ENDOGENOUS COMPOUNDS. THIS ISOZYME DISPLAYS ACTIVITY TOWARD  
 CC SEVERAL CLASSES OF XENOBIOTIC SUBSTRATES: EUGENOL, 4-  
 CC METHYLLUMBELLIFERONE, P-NITROPHENOL, 1-NAPHTHOL, P,P'-BIPHENOL,  
 CC NARINGENIN AND O,O'-BIPHENOL. ACTIVE ALSO ON 3A-HYDROXY AND 17B-  
 CC HYDROXY POSITIONS OF STEROIDS.  
 CC -!- FUNCTION: CONTRIBUTES TO THE FORMATION OF ANDROGEN GLUCURONIDE IN  
 CC EXTRAHEPATIC STEROID TARGET TISSUES SUCH AS THE PROSTATE.  
 CC -!- CATALYTIC ACTIVITY: UDP-glucuronate + acceptor = UDP + acceptor  
 CC beta-D-glucuronoside.  
 CC -!- SUBCELLULAR LOCATION: Microsomal (By similarity).  
 CC -!- TISSUE SPECIFICITY: EXPRESSED IN LIVER, OVARY, PROSTATE, COLON,  
 CC KIDNEY, PANCREAS, BRAIN, CEREBELLUM, MAMMARY GLAND AND EPIDIDYMIS.  
 CC NOT EXPRESSED IN SMALL INTESTINE, SPLEEN, BLADDER, ADRENAL GLAND  
 CC AND TESTIS.  
 CC -!- SIMILARITY: Belongs to the UDP-glycosyltransferase family.  
 CC -----  
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 CC -----  
 DR EMBL; AF112112; AAD24435.1; -.  
 DR InterPro; IPR002213; UDP\_gluco\_trans.  
 DR Pfam; PF00201; UDPGT; 1.  
 DR PROSITE; PS00375; UDPGT; 1.  
 KW Transferase; Glycosyltransferase; Glycoprotein; Transmembrane; Signal;  
 KW Multigene family; Microsome.  
 FT SIGNAL 1 21 POTENTIAL.  
 FT CHAIN 22 528 UDP-GLUCURONOSYLTRANSFERASE 2B19.  
 FT TRANSMEM 493 513 POTENTIAL.  
 FT CARBOHYD 315 315 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SQ SEQUENCE 528 AA; 60741 MW; 3BFD2AE714A27AEE CRC64;

Query Match 24.0%; Score 664.5; DB 1; Length 528;  
 Best Local Similarity 33.2%; Pred. No. 1.5e-44;  
 Matches 168; Conservative 89; Mismatches 218; Indels 31; Gaps 12;

Qy 34 SHYLLMDRVSQILQDHGHNVTMLNHKRG-----PFMPDFKKEEKSYQVISWLAPEDHQREF 89  
 ||:: : : | |||| : | | | : : :  
 Db 34 SHWMNIKTILDELVQRGHEVTVLAYSTSILPDPNPNPSPLKFEICPTSLTETEFQDSVTQL 93  
 Qy 90 KKSFDFFLEETLGGRGKFENLLNVLEYLALQ-----CSHFLNRKDIMDSLKNENFDMV 142

Db 94 VKRWSDIRKDTF-----WPHFLHVQEMMWTYGDMIRKFCKDVVSNNKKLMKKLQESRFDVV 148  
 Qy 143 IVETFDYCPFLIAEKLKGPFVAILSTSEFG-SLE---FGLPIPLSYVPVFRSLTDMDFW 198  
 : : | :|| | || | | :|| | | |||| | | | |  
 Db 149 LADAIAPCGELLAELLKIPFVYSLRFSPGYALEKHGGGFLFPSPSYVPVTMSELRDQMTFM 208  
 Qy 199 GRVKN--FLMFFSFCRRQQHMQSTFDNTIKEHFTGSRPVLSHLLLKAEWFINSDFAFD 256  
 ||:| ::::| | : :: :| : | | :| ||:| | : : |  
 Db 209 ERVQNMIYMVYFDFWFQVWDVKN-WDQFYSK--VLGRPTTLFEIMAKAEIWLIRNYWDFQ 265  
 Qy 257 FARPLLNTVYVGGLMKPIKVPQDLENFIAKFGDSGFVLVTLGSMVNTCQNPFIKEM 316  
 | |||| :||| || ||:|::| | : ||:| | : ||||: : | :  
 Db 266 FPHPLLPNVEFVGGLHCKPAKPLPKEMEETFVQSSGDNGVVVFSLGSMVSN-MSEERANVI 324  
 Qy 317 NNAFAHLPQGVWKCQCSEHWPKDVHLAANVKIVDWLPQSDLLAHPSIRLFTVTHGGQNSIM 376  
 :| | :|| |:: : | | | :| ||||:| | | | :||| | |  
 Db 325 ASALAKIPQKVLWRFDGN---KPDTLGLNTQLYKWLPQNDLLGHPKTRAFITHGGANGIY 381  
 Qy 377 EAIQHGVPVMGIPLEFGDQPENMVRVEAKKFGVSIQLKKLKAETLALKMKQIMEDKRYKSA 436  
 ||| ||:||||:| | ||:| : || | : : | :| :| | ||  
 Db 382 EAIYHGIPMVGVPFLFADQPDNIAHMKAKGAAVRLDFDTMSSTDLLNALKTVINDPIYKEN 441  
 Qy 437 AVAASVILRSHPLSPTQRLVGWIDHVLQTTGGATHLKPYPVFQPPWHEQYLFDFVFLGLT 496  
 | : | | : | | ||:| :| ||: | : : || |||  
 Db 442 AMKLSSIHDQPVKPLDRAVFWIEFVMRHKGAKHLRVAHDLTWFQYHSLDVIGFLLACV 501  
 Qy 497 LGTLWLCGKLLGMAVW-WLRGARKVK 521  
 ::| | || :| :| |  
 Db 502 ATVIFIITKCL-FCVWKFVRTRKKGK 526

# RESULT 13

## UDB9\_MACFA

ID UDB9\_MACFA STANDARD; PRT; 529 AA.  
 AC 002663;  
 DT 15-DEC-1998 (Rel. 37, Created)  
 DT 15-DEC-1998 (Rel. 37, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE UDP-glucuronosyltransferase 2B9 precursor, microsomal (EC 2.4.1.17)  
 DE (UDPGT).  
 GN UGT2B9.  
 OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;  
 OC Cercopithecinae; Macaca.  
 OX NCBI\_TaxID=9541;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Prostate;  
 RX MEDLINE=98030212; PubMed=9364930;  
 RA Belanger G., Beaulieu M., Levesque E., Hum D.W., Belanger A.;  
 RT "Expression and characterization of a novel  
 RT UDP-glucuronosyltransferase, UGT2B9, from cynomolgus monkey."  
 RL DNA Cell Biol. 16:1195-1205(1997).  
 CC -!- FUNCTION: UDPGT IS OF MAJOR IMPORTANCE IN THE CONJUGATION AND  
 CC SUBSEQUENT ELIMINATION OF POTENTIALLY TOXIC XENOBIOTICS AND

CC ENDOGENOUS COMPOUNDS. THIS ISOZYME IS ACTIVE ON C18, C19, AND C21  
 CC STEROIDS, BILE ACIDS, AND SEVERAL XENOBIOTICS INCLUDING EUGENOL,  
 CC 1-NAPHTHOL, AND P-NITROPHENOL.  
 CC -!- CATALYTIC ACTIVITY: UDP-glucuronate + acceptor = UDP + acceptor  
 CC beta-D-glucuronoside.  
 CC -!- SUBCELLULAR LOCATION: Microsomal.  
 CC -!- SIMILARITY: Belongs to the UDP-glycosyltransferase family.  
 CC -----  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL; U91582; AAB50249.1; -.  
 DR InterPro; IPR002213; UDP\_gluco\_trans.  
 DR Pfam; PF00201; UDPGT; 1.  
 DR PROSITE; PS00375; UDPGT; 1.  
 KW Bile acid catabolism; Transferase; Glycosyltransferase; Microsome;  
 KW Signal; Transmembrane; Glycoprotein; Multigene family.  
 FT SIGNAL 1 21 POTENTIAL.  
 FT CHAIN 22 529 UDP-GLUCURONOSYLTRANSFERASE 2B9.  
 FT TRANSMEM 494 514 POTENTIAL.  
 FT CARBOHYD 67 67 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 68 68 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 88 88 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SQ SEQUENCE 529 AA; 60970 MW; F110F85FE3A9DB8D CRC64;

Query Match 24.0%; Score 663.5; DB 1; Length 529;  
 Best Local Similarity 32.9%; Pred. No. 1.8e-44;  
 Matches 169; Conservative 78; Mismatches 220; Indels 47; Gaps 13;

Qy 34 SHYLLMDRVSQILQDHGHNVTML-----NH----KRGPFMPDFKKEE----KSYQ 75  
 ||:: | : : | || ||:| : | | | :  
 Db 34 SHWMNMKTILEELVQRGHEVTVLASSASILFDPNNSSALKIEVFPTSLTKTEFENISMQE 93  
 Qy 76 VISWL-APEDHQREFKKSFDFFLEETLGGRGKFENLLNVLEYLALQCSHFLNRKDIMDSL 134  
 | |: |:| :| : : :| :: | :: | :| |  
 Db 94 VKRWIELPKD-----TFWLYFSQMQEIMWRFGDIIRNF-----CKDVVSNKKLMKKL 140  
 Qy 135 KNENFDMVIVETFDYCPFLIAEKLGPFPVAILSTSFGSLEF-----GLPIPLSYVPVFRS 189  
 : ||:| : | :|| | | : | : | | | | |  
 Db 141 QESRFDVVFADPIFPCELLAELFNIPLVYSLRFTPGYI-FEKHCGGFLFPSPSYVPVMS 199  
 Qy 190 LLTDHMDFWGRVKNFLMFFSF-CRRQQHMQSTFDNTIKEHFTEGSRPVLSHLLLKAELWF 248  
 |:| | | ||| : || | : :| | | | :||::|  
 Db 200 ELSDQMTFMERVKNMIYMLSFDYFQMYDMKKWDQFYSE--VLGRPTTLSETMGKADIWL 257  
 Qy 249 INSDFAFDFARPLLPTVYVGGLMEKPIKPVPQDLENFIAKFGDSGFVLVTLGSMVNTCQ 308  
 | : : | | |||| :||| || ||:|:::| |: ||:| |: :||| |  
 Db 258 IRNSWNFQFPHPLLPNVDFVGLHCKPAKPLPKEMEETFQSSGENGVVVFSLGSMV-TNM 316  
 Qy 309 NPEIFKEMNNAFAHLPQGVWKQCQSHWPKDVHLAANVKIVDWLPQSDLLAHPSIRLFVT 368  
 | : : | | :|| |:| : | | : : |:|:| | | | | :|  
 Db 317 EEERANVIASALAQIPQKVLWRFD---GKKPDTLGLNTRLYKWIPQNDLLGHPKTRAFIT 373

QY 369 HGGQNSIMEAIQHGVPMVGIPFLGDQPENMVRVEAKKFGVSIQLKKLKAETLALKMKQIM 428  
 ||| | | ||| ||||| ||||| |||:|: :: | | : : : || ::| ::  
 Db 374 HGGANGIYEAIYHGVPMVGIPFLFADQPDNIAHMKTKGAAVRLDFDTMSSTDLANRLKTVI 433  
 QY 429 EDKRYKSAAVAASVILRSHPLSPTQRLVGWIDHVLQTGGATHLKPYVFQQPWHEQYLFDV 488  
 | || : | | | : | | | ||: |:: || ||:| | : : ||  
 Db 434 NDPLYKENVMKLSRIQHDQPVKPLDRAVFWIEFVMRHKGAKHLRPAAHDLTWFQYHSLDV 493  
 QY 489 FVFLGLGLTLGLTLWLCLGKLLGMAVWWLRGARKVKE 522  
 ||| ::| | : ||| |:  
 Db 494 IGFLACVATVIFVIMKCCFLFCFW--KFARKGKK 525

RESULT 14

UDBE\_RABIT

ID UDBE\_RABIT STANDARD; PRT; 530 AA.  
 AC P36513;  
 DT 01-JUN-1994 (Rel. 29, Created)  
 DT 01-JUN-1994 (Rel. 29, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE UDP-glucuronosyltransferase 2B14 precursor, microsomal (EC 2.4.1.17)  
 DE (UDPGT) (EGT12).  
 GN UGT2B14.  
 OS Oryctolagus cuniculus (Rabbit).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.  
 OX NCBI\_TaxID=9986;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=New Zealand white; TISSUE=Liver;  
 RX MEDLINE=93315511; PubMed=8325897;  
 RA Tukey R.H., Pendurthi U.R., Nguyen N.T., Green M.D., Tephly T.R.;  
 RT "Cloning and characterization of rabbit liver UDP-  
 RT glucuronosyltransferase cDNAs. Developmental and inducible expression  
 RT of 4-hydroxybiphenyl UGT2B13.";  
 RL J. Biol. Chem. 268:15260-15266(1993).  
 CC -!- FUNCTION: UDPGT is of major importance in the conjugation and  
 CC subsequent elimination of potentially toxic xenobiotics and  
 CC endogenous compounds.  
 CC -!- CATALYTIC ACTIVITY: UDP-glucuronate + acceptor = UDP + acceptor  
 CC beta-D-glucuronoside.  
 CC -!- SUBCELLULAR LOCATION: Microsomal.  
 CC -!- DEVELOPMENTAL STAGE: Expressed primarily in adult rabbits.  
 CC -!- SIMILARITY: Belongs to the UDP-glycosyltransferase family.  
 CC -----  
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 CC -----  
 DR EMBL; L01082; AAA18021.1; -.  
 DR PIR; C47113; C47113.  
 DR InterPro; IPR002213; UDP\_gluco\_trans.

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DR      Pfam; PF00201; UDPGT; 1.
DR      PROSITE; PS00375; UDPGT; 1.
KW      Transferase; Glycosyltransferase; Glycoprotein; Transmembrane; Signal;
KW      Multigene family; Microsome.
FT      SIGNAL          1          24          BY SIMILARITY.
FT      CHAIN           25         530         UDP-GLUCURONOSYLTRANSFERASE 2B14.
FT      TRANSMEM        494        510         POTENTIAL.
FT      CARBOHYD         134        134         N-LINKED (GLCNAC. . .) (POTENTIAL).
FT      CARBOHYD         316        316         N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ      SEQUENCE        530 AA;  60664 MW;  CEAA4BF25B53CB35 CRC64;

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Qy	50	GHNVTMLNLNHRKGPFPDFDKKEEKSQYQVISWLAPEDHQRE-FKKSFDFFLEETLGGRRGKFE	108
Db	51	GHEVIVLRNSASIFIDPSKQANIKFETFPPIAATKDDLEDLFVHYVSTWTNARQNSQWKYF	110
Qy	109	NLLNVL--EY---LALQCSHFLNRKDIMDSLKNENFDMVIVETFDYCPFLIAEKLKGKPFV	163
Db	111	SLLQKLFSEYSDSCENACKEVFNKTLMTKLQESRFDILLSDAIGPCGELLAELLKIPFV	170
Qy	164	AILSTSFG----SLEFGLPIPLSYVPVFRSLLTDHMDFWGRVKNFL--MFFSFCRRQQHM	217
Db	171	YSLRFTPGYTMEKYSGGLSVPPSPYVPIILSDLSGKMTFMERVNNMLCMLYFDFW-FQMFN	229
Qy	218	QSTFDNTIKEHFTEGSRPV-LSHLLLLKAEWFINSDFAFDFARPLLPNTVYVGGLMKPI	276
Db	230	KKRWDQFYSEVL---GRPVTFSSELVGKADMWLIRSYWDLEFPRPTLPNIQFVGGLHCKPA	286
Qy	277	KPVPQDLENFIAKFGDSGFVLVTLGSMVNTCQNPEIFKEMNNAFAHLPGQVIWKQCQSHW	336
Db	287	KPLPKEMEETFVQSSGEEGVVVSFLSGSMVSN-MTEERANLIASAFALPQKVIWRFD---G	342
Qy	337	PKDVHLAANVKIVDWLPQSDLLAHPSIRLFVTHGGQNSIMEAIQHGVPMVGPIPLFGDQPE	396
Db	343	QKPETLGPNTRIYDWIPQNDLLGHPKTKAFVTHGGANGIYEAIHHGIPMVGLPLFGEQPD	402
Qy	397	NMVRVEAKKFGVSIQLKKLKAETLALKMKQIMEDKRYKSAAVAASVILRSHPLSPTQRLV	456
Db	403	NIAHMTAKGAIRLNWKTMSSEDLLNALKTVINDPSYKENVMTLSSIHHQPMKPLDRAV	462
Qy	457	GWIDHVLQTTGGATHLKPYVFQQPWHEQYLFDFVFLGLTLGLTLWL	502
Db	463	FWIEYVMRHKGAKHLRVAAHDLTWFOYHSLDVVGFLVSCAAFLIFL	508

GN UGT2B4 OR UGT2B11.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Liver;  
 RX MEDLINE=87241362; PubMed=3109396;  
 RA Jackson M.R., McCarthy L.R., Harding D., Wilson S., Coughtrie M.W.H.,  
 RA Burchell B.;  
 RT "Cloning of a human liver microsomal UDP-glucuronosyltransferase  
 RT cDNA.";  
 RL Biochem. J. 242:581-588(1987).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Liver;  
 RX MEDLINE=93326164; PubMed=8333863;  
 RA Jin C.-J., Miners J.O., Lillywhite K.J., McKenzie P.I.;  
 RT "cDNA cloning and expression of two new members of the human liver  
 RT UDP-glucuronosyltransferase 2B subfamily.";  
 RL Biochem. Biophys. Res. Commun. 194:496-503(1993).  
 RN [3]  
 RP SEQUENCE FROM N.A., VARIANT GLU-458, AND CHARACTERIZATION.  
 RX MEDLINE=99303261; PubMed=10376768;  
 RA Levesque E., Beaulieu M., Hum D.W., Belanger A.;  
 RT "Characterization and substrate specificity of UGT2B4 (E458): a  
 RT UDP-glucuronosyltransferase encoded by a polymorphic gene.";  
 RL Pharmacogenetics 9:207-216(1999).  
 RN [4]  
 RP SEQUENCE FROM N.A., AND VARIANTS LEU-109 AND LEU-396.  
 RA McKenzie P.I.;  
 RL Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.  
 RN [5]  
 RP SEQUENCE FROM N.A.  
 RA Riedy M., Miller A.;  
 RT "Genomic organization and structure of the UGT2B gene complex at human  
 RT chromosome 4q13.";  
 RL Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.  
 RN [6]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Liver;  
 RX MEDLINE=22388257; PubMed=12477932;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Uzdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length  
 RT human and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 CC -!- FUNCTION: UDPGTs are of major importance in the conjugation and  
 CC subsequent elimination of potentially toxic xenobiotics and  
 CC endogenous compounds. This isozyme is active on polyhydroxylated  
 CC estrogens (such as estriol, 4-hydroxyestrone and 2-hydroxyestriol)  
 CC and xenobiotics (such as 4-methylumbelliferone, 1-naphthol, 4-  
 CC nitrophenol, 2-aminophenol, 4-hydroxybiphenyl and menthol). It is  
 CC capable of 6 alpha-hydroxyglucuronidation of hyodeoxycholic acid.  
 CC -!- CATALYTIC ACTIVITY: UDP-glucuronate + acceptor = UDP + acceptor  
 CC beta-D-glucuronoside.  
 CC -!- SUBCELLULAR LOCATION: Microsomal.  
 CC -!- SIMILARITY: Belongs to the UDP-glycosyltransferase family.  
 CC -!- CAUTION: REF.2 THOUGHT THAT THIS WAS A NEW FORM (UGT2B11). THE  
 CC NAME UGT2B11 HAS NOW BEEN REUSED FOR ANOTHER HUMAN ENZYME.  
 CC -----  
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 CC -----  
 DR EMBL; Y00317; CAA68415.1; -.  
 DR EMBL; AF064200; AAC95002.1; -.  
 DR EMBL; AJ005162; CAA06396.1; -.  
 DR EMBL; AF081793; AAC32272.1; -.  
 DR EMBL; AF135416; AAF78145.1; -.  
 DR EMBL; BC026264; AAH26264.1; -.  
 DR PIR; JN0619; JN0619.  
 DR Genew; HGNC:12553; UGT2B4.  
 DR MIM; 600067; -.  
 DR GO; GO:0005792; C:microsome; NAS.  
 DR GO; GO:0006711; P:estrogen catabolism; IDA.  
 DR GO; GO:0006805; P:xenobiotic metabolism; IDA.  
 DR InterPro; IPR002213; UDP\_gluco\_trans.  
 DR Pfam; PF00201; UDPGT; 1.  
 DR PROSITE; PS00375; UDPGT; 1.  
 KW Transferase; Glycosyltransferase; Glycoprotein; Transmembrane; Signal;  
 KW Multigene family; Microsome; Polymorphism.  
 FT SIGNAL 1 23 BY SIMILARITY.  
 FT CHAIN 24 528 UDP-GLUCURONOSYLTRANSFERASE 2B4.  
 FT TRANSMEM 493 509 POTENTIAL.  
 FT CARBOHYD 315 315 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT VARIANT 109 109 F -> L.  
 FT /FTid=VAR\_011328.  
 FT VARIANT 396 396 F -> L.  
 FT /FTid=VAR\_011329.  
 FT VARIANT 458 458 D -> E.  
 FT /FTid=VAR\_007712.  
 FT CONFLICT 171 172 SL -> RP (IN REF. 1).  
 FT CONFLICT 291 293 EME -> KWK (IN REF. 4).

FT CONFLICT 382 387 EAIYHG -> KAISPR (IN REF. 1).  
SQ SEQUENCE 528 AA; 60512 MW; 6B45E6769971A078 CRC64;

Query Match 23.9%; Score 661.5; DB 1; Length 528;  
Best Local Similarity 34.2%; Pred. No. 2.5e-44;  
Matches 173; Conservative 87; Mismatches 215; Indels 31; Gaps 15;

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Qy      34 SHYLLMDRVSQILQDHGHNVTMLNHKRG----PFMPDFKKEEKSYQVISWLAPEDHQREF 89
      ||:: : : | || ||:| | | | | :: || ::
Db      34 SHWMNIKTILDELVQRGHEVTVLASSASISFDPNSTLKFVYVPVSLTKTEFEDIKQL 93

Qy      90 KKSFDFFLEETLGGRGKFENLLNVL----EYLALQCSHFLNRKDIMDSLKNENFDMVIVE 145
      | : ::| | : :: : | | :: | :| | : ||:: :
Db      94 VKRWAE LPKDTFW--SYFSQVQEIMWTFNDILRKFCCKDIVSNKKLMKKLQESRFDVVLAD 151

Qy     146 TFDYCPF--LIAEKLGPVFVAILSTSEFG-SLE---FGLPIPLSYVPVFRSLLTDHMDFWG 199
      || |::| | || | | | :| || | |||| | :| | |
Db     152 A--VFPPGELLAELLKIPFVYSLRSPGYAIEKHSGGLLFPPSYVPVVMSELSDQMTFIE 209

Qy     200 RVKN--FLMFFSFCRRQQHMQSTFDNTIKEHFTEGSRPVLSHLLLKAELWFINSDFAFDF 257
      |||| ::::| | : | : :| | | | : ||::| | : : | |
Db     210 RVKNMIYVLYFEFWFQIFDMKK-WDQFYSE--VLGRPTTLSETMAKADIWLIRNYWDFQF 266

Qy     258 ARPLLNPNTVYVGGLMEKPIKVPQDLENFIAKFGDSGFVLVTLGSMV-NTCQNPEIFKEM 316
      |||| :||| || ||::::| | : |::| | : :||| || : | :
Db     267 PHPLLPNVEFVGGLHCKPAKPLPKEMEEFVQSSGENGVVVFSLGSMVSNTSE--ERANVI 324

Qy     317 NNAFAHL PQGVIWKQCQSHWPKDVHLAANVKIVDWLPQSDLLAHPSIRLFVTHGGQNSIM 376
      :| | :|| |:: : | | | : : |::||| || | :||| | |
Db     325 ASALAKIPQKVLWRFDGN---KPDTLGLNTRLYKWIPQNDLLGHPKTRAFITHGGANGIY 381

Qy     377 EAIQHGVPMVGIPLFQDQPENMVRVEAKKFGVSIQLKKLKAETLALKMKQIMEDKRYKSA 436
      ||| ||::|||:||| ||::| :::| ||: : : | :| :: | ||
Db     382 EAIYHGIPMVGVPFLFADQPDNIAHMKAKGA AVSLDFHTMSSTDLLNALKTVINDPLYKEN 441

Qy     437 AVAASVILRSHPLSPTQRLVGWIDHVLQTGGATHLKPYVFQQPWHEQYLFDFVFVLLGLT 496
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Db     442 AMKLSRIHHDQPVKPLDRAVFWIEFVMRHKGAKHLRVA AHDLTWFYHSLDVTGFLACV 501

Qy     497 LGTLWL CGKLLGMAVW-WLRGARKVK 521
      ::: | | || ::| :| |
Db     502 ATVIFIITKCL-FCVWKFVRTGKKGK 526
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Search completed: May 7, 2004, 17:31:50  
Job time : 19 secs